



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 103553

TO: Sharon Turner
Location: CM1/10B09&10B19
Art Unit : 1647
Friday, September 12, 2003

Case Serial Number: 09/978191

From: P. Sheppard
Location: Biotech-Chem Library
CM1-1E03
Phone: (703) 308-4499

sheppard@uspto.gov

Search Notes

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103553

From: Turner, Sharon
Sent: Wednesday, September 10, 2003 1:19 PM
To: STIC-Biotech/ChemLib
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Please search CDB and interference files

AA SEQ ID NO:506

Sharon L. Turner, Ph.D.
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CM1-10B09
Mailroom 10B19
Biotechnology GAU 1647
(703) 308-0056

Point of Contact
P. Sheppard
Telephone number: (703) 308-4499

Searcher: _____
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TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2003, 17:10:02; Search time 95 Seconds
(without alignments)
741.562 Million cell updates/sec

Title: US-09-978-191A-506
Perfect score: 1505
Sequence: 1 MRGSOEVLMLVLAIVAGVT.....SQIISFLFEQIGSCSCKKDS 273

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_23:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp Vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_virus:*
 - 16: sp_bacteriap:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1505	100.0	273	Q96EG0	Q96EG0 homo sapien
2	1504	99.9	273	Q9UHF1	Q9UHF1 homo sapien
3	1180	78.4	278	Q9QX15	Q9QX15 mus musculu
4	1103.5	73.3	265	Q9DDCP5	Q9DDCP5 mus musculu
5	727.5	48.3	190	Q9JFKW3	Q9JFKW3 rattus norv
6	435.5	28.9	293	Q35447	Q35447 mus musculu
7	423.5	28.1	293	Q99944	Q99944 homo sapien
8	420.5	27.9	293	Q81V30	Q81V30 homo sapien
9	277.5	18.4	509	Q9VZD0	Q9VZD0 dirosophila
10	277.5	18.4	512	Q95RQ1	Q95RQ1 dirosophila
11	256	17.0	1574	Q88281	Q88281 rattus norv
12	255.5	16.8	558	Q9UJF6	Q9UJF6 homo sapien
13	251.5	16.7	553	Q9NZL7	Q9NZL7 homo sapien
14	251.5	16.7	553	Q81UX8	Q81UX8 homo sapien
15	251.5	16.7	554	Q9NY67	Q9NY67 homo sapien
16	249.5	16.6	553	Q8NBV0	Q8NBV0 homo sapien

Result No.	Score	Query Match	Length	DB ID	Description
17	245.5	16.3	327	Q8BPM8	Q8BPM8 mus musculu
18	245.5	16.3	550	Q9JZ75	Q9JZ75 mus musculu
19	225.5	15.0	544	Q8AVH7	Q8AVH7 xenopus lae
20	223	14.8	561	Q91V88	Q91V88 mus musculu
21	218.5	14.5	578	Q91ZD3	Q91ZD3 mus musculu
22	218	14.5	1664	Q9TVQ2	Q9TVQ2 caenorhabdi
23	217.5	14.5	528	Q9CXDP8	Q9CXDP8 mus musculu
24	198	13.2	747	Q8VHP4	Q8VHP4 mus musculu
25	198	13.2	1004	Q8CCG7	Q8CCG7 mus musculu
26	198	13.2	1034	Q8VHL7	Q8VHL7 mus musculu
27	197.5	13.1	592	Q91XLS	Q91XLS mus musculu
28	196	13.0	1034	Q8V1K5	Q8V1K5 mus musculu
29	194.5	12.9	590	Q8C088	Q8C088 mus musculu
30	193	12.8	609	Q92375	Q92375 mus musculu
31	189	12.6	4	Q14393	Q14393 homo sapien
32	185.5	12.3	1600	Q8K4G0	Q8K4G0 mus musculu
33	185.5	12.3	1666	Q8K4G1	Q8K4G1 mus musculu
34	184.5	12.3	2906	Q9W0H9	Q9W0H9 rattus norv
35	184	12.2	673	Q61592	Q61592 mus musculu
36	184	12.2	674	Q99K57	Q99K57 mus musculu
37	183.5	12.2	784	Q8BM43	Q8BM43 mus musculu
38	183.5	12.2	816	Q8R417	Q8R417 rattus norv
39	183.5	12.2	858	Q8BM06	Q8BM06 mus musculu
40	182.5	12.1	815	Q96J52	Q96J52 homo sapien
41	181.5	12.1	648	Q9VJU4	Q9VJU4 dirosophila
42	181.5	12.0	648	Q9NKD7	Q9NKD7 dirosophila
43	181	12.0	299	Q8BX64	Q8BX64 mus musculu
44	181	12.0	1764	Q35806	Q35806 rattus norv
45	181	12.0	2809	Q96Jp8	Q96Jp8 homo sapien

ALIGNMENTS

RESULT 1

ID	Q96EG0	PRELIMINARY:	PRT:	273 AA.
AC	Q96EG0:			
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-MAR-2003 (TREMBLrel. 23, Last annotation update)			
DE	Similar to NR01 protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxId=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	TISSUE=Ovary;			
RA	Strausberg R.;			
RU	Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC012377; AAH12377.1; -			
DR	InterPro; IPR00152; Asx_Hydroxyl.			
DR	InterPro; IPR001881; EGF_Ca.			
DR	InterPro; IPR006209; EGF_Like.			
DR	Pfam; PF00008; EGF_2.			
DR	SMART; SM00179; EGF_CA_1.			
DR	PROSITE; PS00010; ASX_HYDROXYL; 1.			
DR	PROSITE; PS00022; EGF_1; 1.			
DR	PROSITE; PS01186; EGF_2; 1.			
DR	PROSITE; PS01187; EGF_CA; 1.			
KW	EGF-like domain.			
SK	SEQUENCE 273 AA; 29631 MW; SMD0A4845ED5B868 CRC64;			

Query Match 100.0%; Score 1505; DB 4; Length 273;
Best Local Similarity 100.0%; Pred. No. 1.5e-127;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MRGSOEVLMLVLAIVAGVTENHARRRRCVARRAHGDPVSEFVQVNOPELITTCGHR	60
Db	1	MRGSOEVLMLVLAIVAGVTENHARRRRCVARRAHGDPVSEFVQVNOPELITTCGHR	60
Qy	61	ACTYRTYRTAARSRPGLAPRRPVACCPGMKRTSGLPGACGAALIQPCRNGSCVQP	120

Db 1
 61 ACSTYRTTYRTAYRRSPGLAPARPRVYACCGMKTSGLPAGCAAIICOPPCRRNGSCVOP 120
 OY 121 GRCPCPAGMGDPDTQOSVDDECSARRGSGPCRCINTAGSYWCOCMEGHSISADGTLCPVK 180
 Db 121 GRCPCPAGMGDPDTQOSVDDECSARRGSGPCRCINTAGSYWCOCMEGHSISADGTLCPVK 180
 OY 181 GPPRVANPPTGVDSAMKEEVORLQSRVDLLEEKQLQVLAPLHSLASQALEHGLPDPGSL 240
 Db 181 GPPRVANPPTGVDSAMKEEVORLQSRVDLLEEKQLQVLAPLHSLASQALEHGLPDPGSL 240
 OY 241 VHSFOQLGRIDSLSEQISFLIEQLGSCCKXDS 273
 Db 241 VHSFOQLGRIDSLSEQISFLIEQLGSCCKXDS 273

RESULT 2

O9UHFL PRELIMINARY; PRT; 273 AA.
 ID G9UHFL
 AC G9UHFL
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 GN NOTCH4-like protein (Hypothetical protein).
 OS ZNEU1 OR DKFZP58612317.
 OC Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shepard P., Jelinek L., Whitmore T., Blumberg H., Lehner J.,
 RA O'Hara P.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Koehrer K., Beyer A., Nemes H.W., Gassenhuber J., Wiemann S.,
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF186111; AAF01439.1; -
 DR EMBL; AL512735; CAC21666.1; -
 DR HSSP; P08709.1PAK.
 DR InterPro; IPR000152; Aex_hydroxyl.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR Pfam; PF00008; EGF_2.
 DR SMART; SM00179; EGF_CA; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS01187; EGF_CA; 1.
 KW Hydroxylase domain.
 SQ SEQUENCE 273 AA; 29617 MW; 5740BB845BD5A988 CRC64;

Query Match

Best Local Similarity 99.8%; Score 1504; DB 4; Length 273;
 Matches 272; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRGSGQEVLLMMLVLAAGG-TEHAYRGRVCAVRAHGPVSSFFQRYVYQPLTTCDGH 60
 Db 1 MRGSGQEVLLMMLVLAAGGTEHAYRGRVCAVRAHGPVSSFFQRYVYQPLTTCDGH 60
 OY 61 ACSTYRTTYRTAYRRSPGLAPARPRVYACCGMKTSGLPAGCAAIICOPPCRRNGSCVOP 120
 Db 61 ACSTYRTTYRTAYRRSPGLAPARPRVYACCGMKTSGLPAGCAAIICOPPCRRNGSCVOP 120
 OY 121 GRCPCPAGMGDPDTQOSVDDECSARRGSGPCRCINTAGSYWCOCMEGHSISADGTLCPVK 180
 Db 121 GRCPCPAGMGDPDTQOSVDDECSARRGSGPCRCINTAGSYWCOCMEGHSISADGTLCPVK 180
 OY 181 GPPRVANPPTGVDSAMKEEVORLQSRVDLLEEKQLQVLAPLHSLASQALEHGLPDPGSL 240
 Db 181 GPPRVANPPTGVDSAMKEEVORLQSRVDLLEEKQLQVLAPLHSLASQALEHGLPDPGSL 240

OY 241 VHSFOQLGRIDSLSEQISFLIEQLGSCCKXDS 273
 Db 241 VHSFOQLGRIDSLSEQISFLIEQLGSCCKXDS 273

RESULT 3

O9QXTS PRELIMINARY; PRT; 278 AA.
 ID O9QXTS
 AC O9QXTS
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DE 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 GN NOTCH4-like protein (Vascular endothelial zinc finger 1).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shepard P., Jelinek L., Whitmore T., Blumberg H., Lehner J.,
 RA O'Hara P.;
 RL "Mus musculus homolog of HLA class III region containing NOTCH4
 gene."
 RT Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Presnell S., Gilbert T., Whitmore T., Foster D., Hart C., Lehner J.,
 RA Martinez T., Hoffman R., O'Hara P.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF184973; AAF01322.1; -
 DR EMBL; BC024610; AAH24610.1; -
 DR HSSP; P00740.1EDM.
 DR MED; MGI:1313291; Vezfl.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR006210; IEGF.
 DR Pfam; PF00008; EGF_2.
 DR SMART; SM00181; EGF_1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS01187; EGF_CA; 1.
 KW EGF-like domain.
 SQ SEQUENCE 278 AA; 30125 MW; 863159F567102FA7 CRC64;

Query Match

Best Local Similarity 78.4%; Score 1180; DB 11; Length 278;
 Matches 213; Conservative 19; Mismatches 40; Indels 2; Gaps 2;

OY 1 MRGSGQEVLLMMLVLAAGG-TEHAYRGRVCAVRAHGPVSSFFQRYVYQPLTTCDGH 59
 Db 4 MRGSGQEVLLMMLVLAAGGTEHAYRGRVCAVRAHGPVSSFFQRYVYQPLTTCDGH 63
 OY 60 RACSTYRTTYRTAYRRSPGLAPARPRVYACCGMKTSGLPAGCAAIICOPPCRRNGSCVOP 119
 Db 64 RACSTYRTTYRTAYRRSPGLAPARPRVYACCGMKTSGLPAGCAAIICOPPCRRNGSCVOP 123
 OY 120 GRCPCPAGMGDPDTQOSVDDECSARRGSGPCRCINTAGSYWCOCMEGHSISADGTLCPVK 179
 Db 124 GRCPCPAGMGDPDTQOSVDDECSARRGSGPCRCINTAGSYWCOCMEGHSISADGTLCPVK 183
 OY 180 GPPRVANPPTGVDSAMKEEVORLQSRVDLLEEKQLQVLAPLHSLASQALEHGLPDPGSL 238
 Db 184 GPPRVANPPTGVDSAMKEEVORLQSRVDLLEEKQLQVLAPLHSLASQALEHGLPDPGSL 243
 OY 239 LVVHSFOQLGRIDSLSEQISFLIEQLGSCCKXCKD 272

DB 244 LIAHSFOQLDRIDSLSEOVSFLEHLGSCSCKKD 277

RESULT 4 PRELIMINARY; PRT; 265 AA.

AC Q9DCP5; 01-JUN-2001 (TrEMBLrel. 17, Created)
AC Q9DCP5; 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Vascular endothelial zinc finger 1.
GN VZFL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
MEDLINE=21085660; PubMed=11217651;
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Komno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K. I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H. A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gasteirland T., Glasi C., King B., Kochiwa H.,
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schiml L. M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M. F.,
RA Brownstein M. J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustinich S., Hill D., Hofmann M., Hume D. A., Kamita M., Lee N. H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K. H., Weitz C., Whitlaker C., Williams L.,
RA Wyshak-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RA "Functional annotation of a full-length mouse cDNA collection.";
RT Nature 409:685-690(2001).;
RL EMBL; AK002601; BAB22222.1; -.
DR HSSP; P00740; 1EDM.
DR MGD; MGI:1113291; Vezfl.
DR InterPro; IPR001881; EGF_Ca..
DR InterPro; IPR006209; EGF_like..
DR InterPro; IPR006210; IEGF.
DR Pfam; PF00008; EGF_2.
DR SMART; SM00181; EGF; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA; 1.
KW EGF-like domain.
SQ SEQUENCE 265 AA; 28665 MW; D81EC3DA884FP97E CRC64;

Query Match 73.3%; Score 1103.5; DB 11; Length 265;
Best Local Similarity 73.7%; Pred. No. 2.1e-91;
Matches 202; Conservative 18; Mismatches 39; Indels 15; Gaps 3;

DB 1 MRSQGVLLMLLVAVGG-TEHAYRPGRRVCAVRAHGDPVSESPVQVRYQDFLTTCQGH 59
DB 4 MWGSGELLVAMFLVLAADGTTTEHVYRPSRVCVTVGSGSISSETFQRYVYQDYLTTCQGH 63
OY 60 RACSTYRTTYRATVRSRGLAARPRVYACCPGWRKTSGLRPGAGAAITQPPRRNGSCVQ 119
DB 64 RACSTYRTTYRATVRSRGLAARPRVYACCPGWRKTSGLRPGAGAAITQPPRRNGSCVQ 123
OY 120 PGRRCRPAAGWRRGDTQSDVDECSARRGGCPORCINTAGSYWCQWEGHSLADGTLVCPK 179
DB 124 FGHGRCVPGWGGDTQSDVDECSARRGGCPORCINTAGSYWCQWEGHSPADGTRCLSK 183
OY 180 GGPVAVVAVNPT-GVDSAMKEEVQRLQSRVLDLLEKQLQVLAVLADLHSLASQALEHGLPDPGS 238
DB 184 EGPSVAVAVNPTAVGVSMAREEVYRIQARVAVLEQKQLQVLAVLADLHSLASRSTHGLQDPGS 243

OY 239 LIAHSFOQLDRIDSLSEOVSFLEHLGSCSCKKD 272
DB 244 LIAHSFOQLDRIDSLSEOVSFLEHLGSCSCKKD 264

RESULT 5 PRELIMINARY; PRT; 190 AA.

AC Q9JRW3; 01-OCT-2000 (TrEMBLrel. 15, Created)
AC Q9JRW3; 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE CBL20.
GN CBL20.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Chan M.T.W., Ng C.C.Y., Lim E.K.B., Huynh H.T.;
RT "Cloning and Characterization of a Novel 20.4kD Estrogen-regulated
RT protein in the Rat Spleen.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Marcantonio D., Huynh H.T.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF223678; AAF5352.1; -.
DR InterPro; IPR00152; Asx hydroxyl.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR Pfam; PF00008; EGF; 2.
DR SMART; SM00179; EGF_CA; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA; 1.
KW EGF-like domain.
SQ SEQUENCE 190 AA; 20527 MW; C540EF0687F1E998 CRC64;

Query Match 48.3%; Score 727.5; DB 11; Length 190;
Best Local Similarity 76.9%; Pred. No. 1.1e-57;
Matches 130; Conservative 15; Mismatches 23; Indels 1; Gaps 1;

OY 105 AICPPRCNNGSCVQVGRGCRCPAGWRGDTQSDVDECSARRGGCPORCINTAGSYWCOCW 164
DB 21 AICPPRCNNGSCVQVGRGCRCPAGWRGDTQSDVDECSARRGGCPORCINTAGSYWCOCW 80
OY 165 EGHSLIADGTLVCPKXGPRVAVNPT-GVDSAMKEEVQRLQSRVLDLLEKQLQVLAVLPHS 223
DB 81 EGQSPSADGVLCLEPREGSPVAVPSPTPGVDSVIVREXVYKQLQARVAVLEQKQLQVLAVLPHS 140
OY 224 LASQALEHGLDPPGSLVHVSFOQLGRITSLSEQISFLEHLGSCSCKKD 272
DB 141 LASRPFHGLQDPGSLVHVSFOQLDRIDSLSEOVSFLEHLGSCSCKKD 189
RESULT 6 PRELIMINARY; PRT; 293 AA.
AC Q35447; 01-JAN-1998 (TrEMBLrel. 05, Created)
AC Q35447; 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical 32.1 kDa protein.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

RA . SEQUENCE FROM N.A.
 RA Rowen L., Mahaitas G., Qin S., Ahearn M.E., Dankers C., Lasky S.,
 RA Loretz C., Schmidt S., Tipton S., Traicoff R., Zackroff K., Hood L.,
 RT "Sequence of the mouse major histocompatibility locus class III
 region."
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF030001; AAB82010.1; -
 DR HSSP: P35555; IEMN.
 DR InterPro: IPR001152; Asx hydroxyl.
 DR InterPro: IPR001881; EGF_CA.
 DR Pfam: PF00008; EGF_2.
 DR SMART: SM00179; EGF_CA; 1.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS01187; EGF_CA; 1.
 KW Hypothetical protein; EGF-like domain.
 SQ SEQUENCE 293 AA; 32066 MW; 8X99A5EC00A2C62 CRC64;

Query Match 28.9%; Score 435.5; DB 11; Length 293;
 Best Local Similarity 37.3%; Pred. No. 3.5e-31;
 Matches 112; Conservative 36; Mismatches 101; Indels 51; Gaps 14;

QY 1 MRGSGEVLMLVLAAGV-GTE-HAYRPRRCAVRAHGDV--SESPVQRYVYQPFLLTTC 56
 Db 11 LRG-----LSFFFLVIMTGETRGGSEKESIGVCSKQTLVPLRYVESYSPVYKRYLTLG 65
 QY 57 DGRHAGSTYRTYRTYRNSPGLAPRPRVYACCPGKRTSGLPGACGA-AIQPPRCNGG 115
 Db 66 AGRRICTYRTYRNVREVRVPR-QTHVYVCCQGWKPKH--FGALYTDALCSKPCINNG 122
 QY 116 SCVQPRGRCPCPAGMRSDTQSPVDECSARGGCPQRCINTAGSYWCQWEGHSLSDAGTL 175
 Db 123 VCTGPRRCPCAPGKCHVDVDCRSLTLCSHGCLMNTLGSFLCSCPHPIVYGLDGRF 182
 QY 176 CVPKGGPRVAVNPTGV-----DSAMKEVQRLQSRVLDLEKQLQVLAAP 221
 Db 183 CA--GGPPE--SPYSASTLVAVREADSEERALRVEVLELRLEKQLQ----- 228
 QY 222 HSLAQA--LEHGPR-DPGLSLVHSPQQL-----GRIDLSLSEQISFLERQIGSCSKKDS 273
 Db 229 --WATQAGAWVRAVLPMPPELRPEQVAVLWGRDRLTESLSDVLLLEERLQACACEDNS 286

RESULT 7
 O99944 PRELIMINARY; PRT; 293 AA.
 AC O99944.
 DT 01-MAR-1997 (TREMBlrel. 03, Created)
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE NG3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCB1_TaxID=9606;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA Rowen L., Dankers C., Baskin D., Faust J., Loretz C., Ahearn M.E.,
 RA Banta A., Spies T., Hood L.,
 RT "Sequence determination of 300 kilobases of the human class III MHC
 locus."
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U99336; AAB47494.1; -
 DR HSSP: P35555; IEMN.
 DR GeneW: HGNC:13944; Coort8.
 DR InterPro: IPR000152; Asx hydroxyl.
 DR InterPro: IPR001881; EGF_CA.
 DR Pfam: PF00008; EGF_2.
 DR SMART: SM00179; EGF_CA; 1.

DR PROSITE: PS00010; ASX HYDROXYL; 1.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS01187; EGF_CA; 1.
 KW EGF-like domain.
 SQ SEQUENCE 293 AA; 32262 MW; 6519CA254FB23FD0 CRC64;

Query Match 28.1%; Score 423.5; DB 4; Length 293;
 Best Local Similarity 36.5%; Pred. No. 4.2e-30;
 Matches 103; Conservative 37; Mismatches 107; Indels 35; Gaps 10;

QY 12 LVLAVGTEHAYRPRRCAVRAHGDV--SESPVQRYVYQPFLLTTCGHRACSTYRTY 69
 Db 19 LLIPGEGAKGSLRESGVCSKQTLVPLRYVESYSPVYKRYLTLGARRICSTYRTMY 78
 QY 70 RTAYRSPGLAPRPRVYACCPGKRTSGLPGA--CGAALICPPRCNAGSCVQPRCPCPA 127
 Db 79 RVMW-REVRREVOQTHAVCCQGWKPKH--FGALTC-EAICAKPCLNGVAVCRPDQCECAP 134
 QY 128 GMRGDTQSDVDECSARAGGCPQRCINTAGSYWCQWEGHSLSDAGTLVCPKGGPRVAVP 187
 Db 135 GMGGKHCHVDVDCRSTLTLCSHCCFNTAGSFTGCGPHDVLVGDGRTCWEGSPPEPTSA 194
 QY 188 NPTGV-----DSAMKEVQRLQSRVLDLEKQLQVLAAPLHSLAQA--LEHGPR-D 235
 Db 195 SILSVAVRAEKDERALKQETHELGRLERLDQ-----WAGQAGAWVRAVLPVP 243
 QY 236 PGLSLVHSPFOQL-----GRIDLSLSEQISFLERQIGSCSKKDS 273
 Db 244 PEEIQPEQVAVLWGRDRLTESLSDVLLLEERLQACACEDNS 285

RESULT 8
 Q81V30 PRELIMINARY; PRT; 293 AA.
 ID Q81V30.
 AC Q81V30.
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Chromosome 6 open reading frame 8.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCB1_TaxID=9606;
 RX [1]
 RP SEQUENCE FROM N.A.
 RA Tissue=Brain;
 RA Strausberg R.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC035574; AAB35574.1; -
 DR SQUENCE 293 AA; 32261 MW; 6519CA25568FFD0 CRC64;

Query Match 27.9%; Score 420.5; DB 4; Length 293;
 Best Local Similarity 36.2%; Pred. No. 7.7e-30;
 Matches 102; Conservative 38; Mismatches 107; Indels 35; Gaps 10;

QY 12 LVLAVGTEHAYRPRRCAVRAHGDV--SESPVQRYVYQPFLLTTCGHRACSTYRTY 69
 Db 19 LLIPGEGAKGSLRESGVCSKQTLVPLRYVESYSPVYKRYLTLGARRICSTYRTMY 78
 QY 70 RTAYRSPGLAPRPRVYACCPGKRTSGLPGA--CGAALICPPRCNAGSCVQPRCPCPA 127
 Db 79 RVMW-REVRREVOQTHAVCCQGWKPKH--FGALTC-EAICAKPCLNGVAVCRPDQCECAP 134
 QY 128 GMRGDTQSDVDECSARAGGCPQRCINTAGSYWCQWEGHSLSDAGTLVCPKGGPRVAVP 187
 Db 135 GMGGKHCHVDVDCRSTLTLCSHCCFNTAGSFTGCGPHDVLVGDGRTCWEGSPPEPTSA 194
 QY 188 NPTGV-----DSAMKEVQRLQSRVLDLEKQLQVLAAPLHSLAQA--LEHGPR-D 235
 Db 195 SILSVAVRAEKDERALKQETHELGRLERLDQ-----WAGQAGAWVRAVLPVP 243
 QY 236 PGLSLVHSPFOQL-----GRIDLSLSEQISFLERQIGSCSKKDS 273

244 PEELOPEVALWGRGDRISLSDVLLQERLQACSCEDNS 285

RESULT 9 PRELIMINARY; PRT; 509 AA.
Q9VZD0 Q9VZD0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE CG7447 protein.
GN CG7447.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Ephydroidea; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
SEQUENCE FROM N.A.
RA STRAIN=BERKELEY;
RA MEDLINE=20196606; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amaratides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borokva D., Botchan M.R., Bouck J., Brockstein P., Broctier P.,
RA Burtis K.C., Busan D.A., Butler H., Cadiet E., Center A., Chandra I.,
RA Chery J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dieter S.M.,
RA Dodson K.L., Dopp L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dudin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
RA Fogler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hootin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jatali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,
RA Lasop P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Maltel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mcelroy G., Milhina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclib J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shee B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svarek R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL; AE003481; AAF47894.1; -
DR HSSP; P00740; 1EDM.
DR FLYBase; FBgn0035539; CG7447.
DR InterPro; IPR000152; Aex_hydroxyl.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_Like.
DR Pfam; PF00008; EGF_2.
DR SMART; SM00179; EGF_CA; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
KW EGF-like domain.

SEQ SEQUENCE 509 AA; 57413 MW; FE4782E4A6E121F0 CRC64;
Query Match 18.4%; Score 277.5; DB 5; Length 509;
Best Local Similarity 27.8%; Pred. No. 1.1e-16;
Matches 73; Conservative 40; Mismatches 113; Indels 37; Gaps 9;
QY 28 RRVCAVRAHGDPPV--SESPVQRYVQPEPLTTC-----GHRACSTYRTYRTAYRRSPGIA 80
DB RHICQQRVTMPVVRTEVRSRPTWKHVAATCCQPEPTFGQCTRVQVVHEDQAYRVIDHK 301
QY 81 PARP-RYACCCGKWKRTSLPGACCAATCQPPCRNGSCVQGRKCRCPAGMGDTQGSVD 139
DB TAQQMTYDCCGWSNENRSDSCMKRPTCSARCONGNCTAPSTGSCPTGFTGRFCEQDVP 361
QY 140 ECSARRGCGPCRCINTAGSYWCCQCEHSHLSADGTLVCPKGGPPRVAPN-----P 189
DB ECQTEK-PCDQCCINTHGSYFCRCRQGVLVSDQSC-----KVSFNADDAFARPLE 414
QY 190 TGVDSPAMKEEVQRLQS-----RVLDLEKQLQVLAFLHSLASQ--ALEHGLPDPG 237
DB NDIDDTDAEVAFLRQKTEKSLANERVHTELQKSLQATYSVVDTLKSLSTLEKQAOQVDS 474
QY 238 SLLVHSFQQLGRIDSLSEQISFL 260
DB 475 RLQNTLVYKTESRTYKLEGMNL 497
RESULT 10
Q95RQ1 PRELIMINARY; PRT; 512 AA.
AC Q95RQ1;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE LD16414p.
GN CG7447.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
SEQUENCE FROM N.A.
RA STRAIN=BERKELEY;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Fartan D., Frise E., George R.,
RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nuno J., Paclib J., Pargagas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY061220; AA128768.1; -
DR FLYBase; FBgn0035539; CG7447.
DR InterPro; IPR000152; Aex_hydroxyl.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_Like.
DR Pfam; PF00008; EGF_2.
DR SMART; SM00179; EGF_CA; 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS01187; EGF_CA; 1.
KW EGF-like domain.
SO SEQUENCE 512 AA; 57770 MW; 4DD372E4A6E7627 CRC64;
Query Match 18.4%; Score 277.5; DB 5; Length 512;
Best Local Similarity 27.8%; Pred. No. 1.1e-16;
Matches 73; Conservative 40; Mismatches 113; Indels 37; Gaps 9;
QY 28 RRVCAVRAHGDPPV--SESPVQRYVQPEPLTTC-----GHRACSTYRTYRTAYRRSPGIA 80
DB RHICQQRVTMPVVRTEVRSRPTWKHVAATCCQPEPTFGQCTRVQVVHEDQAYRVIDHK 304
QY 81 PARP-RYACCCGKWKRTSLPGACCAATCQPPCRNGSCVQGRKCRCPAGMGDTQGSVD 139

Db 305 TQAQMTYDCCTGMSNENRPSDSCMKPICSARCGNGANTASTGSCPTGPFGRFCBDDVD
 Qy 140 FBSARAGGCPORCINTAGSYWCQCEGHSLSADGTLVCPKGGPPRVAPN-----P 189
 Db 365 BCYTEK-PDDOCCINTHGSYFCRCRQGFVLOSDDQSC-----KXSVTNADAPPEARBLE 417
 Qy 190 TGVDSAMKEVQRLQS-----RVDLLEBKLVAVLAPLHLSAQ--ALEFGLDPPG 237
 Db 418 NDIDDTDAEVAFLRLOKIKRSLANRVTNBLQKSLQATYVAVDTLKRSLSTLEKQADVS 477
 Qy 238 SLVHSPQQLGRIDLSLSEQISFL 260
 Db 478 RLQTNLYKTERSTRNKLQEGMNLML 500

RESULT 11
 088281
 ID 088281 PRELIMINARY; PRT; 1574 AA.

AC 088281
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE MEGP6.
 OS MEGP6.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCB1_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=98360089; PubMed=9693030;
 RA Nakayama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara O.;
 RT "Identification of high-molecular-weight proteins with multiple EGF-
 like motifs by motif-trap screening.";
 RL Genomics 51:27-34(1998).
 DR EMBL: AB011532; BAA32462.1; -
 DR HSSP: P00736; IABO.
 DR InterPro: IPR00152; Asx_hydroxyl.
 DR InterPro: IPR01881; EGF_Ca.
 DR InterPro: IPR006209; EGF_like.
 DR InterPro: IPR002049; Laminin_EGF.
 DR Pfam: PF00008; EGF_24.
 DR PRINTS: PR00011; EGF_LAMININ.
 DR SMART: SM00179; EGF_CA; 4.
 DR PROSITE: PS00010; ASX_HYDROXYL; 5.
 DR PROSITE: PS01186; EGF_1; 23.
 DR PROSITE: PS01187; EGF_2; 23.
 DR PROSITE: PS01187; EGF_CA; 5.
 KW EGF-like domain.
 SQ SEQUENCE 1574 AA; 165445 MW; 2848533DBF77F6E7 CRC64;

Query Match 17.0%; Score 256; DB 11; Length 1574;
 Best Local Similarity 37.9%; Pred. No. 3.3e-14;
 Matches 64; Conservative 16; Mismatches 61; Indels 28; Gaps 9;

Qy 30 VCAVVR-----AHGDPVSESEFVQRYVPELITTDGHRAC--STYRTITRYARRSGLAPA 82
 Db 43 VCAEQLKLVGHROPVQAFSRVWPVRTGCAQQAQAMCGERRRIVYMSYQVVA-TTEA 101
 Qy 83 RPRRYACCPGWRKRTSGLPGA-----CGAAI--COPPCRN--GGSCVQGRGCRCPAGMR-- 130
 Db 102 RIVFRCCPQMSQKPGGEGCLSDVDEGASANGGCEGFCNTVGGF-----YCRCPGYDQ 156
 Qy 131 --GPTQGVDECSARAGGCPORCINTAGSYWCQCEGHSLSADGTLV 177
 Db 157 GPGKTCQ-DVDECRANHGCCQHRVCVTPGSIYCECKPGRFRLHTDGRCTL 204

RESULT 12
 09UFK6
 ID 09UFK6 PRELIMINARY; PRT; 558 AA.

AC 09UFK6;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Hypothetical protein (Fragment).
 DN DKFZ564P2063.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Duesterhoert A., Lauber J., Mewes H.W., Gaesshuber J., Wiemann S.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 CC -1 SIMILARITY: CONTAINS 1 MAM DOMAIN.
 DR EMBL: AL117610; CAB56014.1; -
 DR HSSP: P00736; IABO.
 DR Genew; HGNC:3235; EGF6.
 DR InterPro: IPR00152; Asx_hydroxyl.
 DR InterPro: IPR01881; EGF_Ca.
 DR InterPro: IPR006209; EGF_like.
 DR InterPro: IPR009998; MAM_domain.
 DR Pfam: PF00008; EGF; 4.
 DR Pfam: PF00629; MAM; 1.
 DR SMART: SM00179; EGF_CA; 3.
 DR PROSITE: PS00010; ASX_HYDROXYL; 3.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 2.
 DR PROSITE: PS01187; EGF_CA; 2.
 DR PROSITE: PS0060; MAM_2; 1.
 KW Hypothetical protein; EGF-like domain; Glycoprotein.
 FT NON-TER
 SQ SEQUENCE 558 AA; 61828 MW; AA38D7DCE402BFA3 CRC64;

Query Match 16.8%; Score 252.5; DB 4; Length 558;
 Best Local Similarity 36.8%; Pred. No. 2.1e-14;
 Matches 57; Conservative 17; Mismatches 50; Indels 31; Gaps 7;

Qy 58 GHRACSTYRTITRYARRSGLAPARPRVACCPGWRKRTSGLPGACGAATGQPPCRNGGSC 117
 Db 26 GNAASARHHGILASA--RQPGVCHYGTKLACCGMWRNS--KGVG-EATCEPCK-FGGC 79
 Qy 118 VQGRCRCPAGWRDGTQSDVDECSARAGGCPORCINTAGSYWCQCEGHSLSADGTLV 177
 Db 80 VGPWKRCCLRGYTKTCSQDVNDEGCMKPRPCQHRVCVTHGSYKCFCLSGHMLMPAT-CV 138
 Qy 178 -----PKGGP-----RVAPN 188
 Db 139 YSRTCAMINCOVSCEDTEEGPQCLCPSSGRLAPN 173

RESULT 13
 09NZL7
 ID 09NZL7 PRELIMINARY; PRT; 553 AA.

AC 09NZL7
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Epidermal growth factor repeat containing protein.
 DN EGF6.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20079166; PubMed=10610727;
 RA Yeung G., Mulero J.J., Bernitsen R.P., Loeb D.B., Drmanac R.,
 RT "Cloning of a novel epidermal growth factor repeat containing gene
 EGF6: expressed in tumor and fetal tissues.";
 RL Genomics 62:304-307(1999).

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OM protein - protein search, using sw model1

Run on: September 10, 2003, 17:09:17; Search time 23 Seconds
(without alignments)
558,187 Million cell updates/sec

Title: US-09-978-191A-506

Perfect score: 1505

Sequence: 1 MRGSGEVLIMLVLVAVGVT.....SEQISFLEEQIGSCSKKDS 273

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	ID	Description
1	196	13.0	1964	NTC4_MOUSE	P31695 mus musculus
2	188.5	12.5	2003	NTC4_HUMAN	Q99466 homo sapien
3	185	12.3	816	NEL2_MOUSE	Q61220 mus musculus
4	183.5	12.2	2907	FBN2_MOUSE	Q61555 mus musculus
5	182.5	12.1	816	NEL2_HUMAN	Q99435 homo sapien
6	182	12.1	810	NEL1_HUMAN	Q92832 homo sapien
7	180.5	12.0	816	NEL2_RAT	Q62918 rattus norv
8	180	12.0	810	NEL1_RAT	Q62919 rattus norv
9	176.5	11.7	816	NEIL_CHICK	Q90827 gallus gall
10	175.5	11.7	2871	FBN1_HUMAN	P35555 homo sapien
11	175.5	11.7	2871	FBN1_HUMAN	Q9um47 homo sapien
12	175	11.6	652	CD93_HUMAN	Q9nyj3 homo sapien
13	175	11.6	2703	NOTCH_HUMAN	P07207 dirosophila
14	173.5	11.5	1247	NIDO_HUMAN	P14543 homo sapien
15	172.5	11.5	2871	FBN1_MOUSE	Q61554 mus musculus
16	172	11.4	2531	NTC1_MOUSE	Q01705 mus musculus
17	171.5	11.4	2871	FBN1_BOVIN	P98133 bos taurus
18	170.5	11.3	6871	FBN1_FIG	Q9v736 sus scrofa
19	170	11.3	2911	FBN2_MOUSE	Q08761 mus musculus
20	170	11.3	2911	FBN2_HUMAN	P35556 homo sapien
21	169.5	11.3	2318	NTC3_MOUSE	Q61982 mus musculus
22	169	11.2	833	DL_DROME	P10041 drosophila
23	168	11.2	675	PRTS_RAT	P53813 rattus norv
24	165	11.0	1238	JAG2_HUMAN	Q92119 homo sapien
25	165	11.0	1247	JAG2_MOUSE	Q9yqes mus musculus
26	164	10.9	1202	JAG2_RAT	P97607 rattus norv
27	164	10.9	1429	LIL2_CAELE	P14585 caenorhabdi
28	164	10.9	2524	NOTC_XENLA	P21783 xenopus lae
29	163.5	10.9	2556	NTC1_HUMAN	P46531 homo sapien
30	163	10.8	644	CD93_MOUSE	Q89103 mus musculus
31	162.3	10.8	2319	NTC3_RAT	Q9t172 rattus norv
32	162	10.8	459	PRTG_PIG	Q991P2 sus scrofa
33	162	10.8	646	PRTS_FABIT	P98118 oryctolagus

ID	Score	Query Match	Query Length	ID	Description
34	162	10.8	833	SRC2_MOUSE	P59222 mus musculus
35	162	10.8	870	SRC2_HUMAN	Q966p6 homo sapien
36	161	10.7	675	PRTS_BOVIN	P07224 bos taurus
37	160.5	10.7	618	DLL3_HUMAN	Q9nyj7 homo sapien
38	160.5	10.7	2531	NTC1_RAT	Q07008 rattus norv
39	160	10.6	2437	NTC1_BRARE	P46530 brachydanio
40	159.5	10.6	643	CD93_RAT	Q96t61 rattus norv
41	158.5	10.5	407	FA7_BOVIN	P22457 bos taurus
42	158.5	10.5	456	PRTG_BOVIN	P00745 bos taurus
43	157.5	10.5	379	FBN1_MOUSE	Q9nu41 mus musculus
44	157	10.4	676	FBN1_HUMAN	P07225 homo sapien
45	156.5	10.4	1213	JAG3_BRARE	Q90y54 brachydanio

ALIGNMENTS

RESULT 1

NTC4_MOUSE STANDARD: PRT, 1964 AA.

AC P31695: Q35442: O88314; O88316; Q62389; Q9R1W9; Q9R1X0;

DT 01-JUL-1993 (Rel. 26, created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Neurogenic locus notch homolog protein 4 precursor (Notch 4)

DE [Contains: Transforming protein Int-3].

GN NOTCH4 OR INT3 OR INT-3.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_TaxID=10090;

LN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=92194507; PubMed=1312643;

RA Robbins J., Blondel B.J., Gallahan D., Callahan R.;

RT "Mouse mammary tumor gene int-3: a member of the notch gene family

RT transforms mammary epithelial cells. ";

RL J. Virol. 66:2594-2599(1992).

LN [2]

RP REVISIONS. SEQUENCE FROM N.A.

RX MEDLINE=97294599; PubMed=9150355;

RA Gallahan D., Callahan R.;

RT "The mouse mammary tumor associated gene INT3 is a unique member of

RT the NOTCH gene family (NOTCH4). ";

RL Oncogene 14:1883-1890(1997).

LN [3]

RP SEQUENCE FROM N.A.

RX TISSUE=Lung, and Testis;

RA MEDLINE=96281668; PubMed=8681805;

RT Uytendaele H., Marazzi G., Wu G., Yan Q., Sassoon D., Kitajewski J.;

RT "Notch4/int-3, a mammary proto-oncogene, is an endothelial

RT cell-specific mammalian Notch gene. ";

RL Development 122:2251-2259(1996).

LN [4]

RP SEQUENCE FROM N.A.

RX Romen L., Mahaitas G., Qin S., Ahearn M.E., Dankers C., Lasky S.,

RA Loretz C., Schmidt S., Tipton S., Traicoff R., Zackrison K., Hood L.;

RT "Sequence of the mouse major histocompatibility locus class III

RT region. ";

RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.

LN [5]

RP SEQUENCE OF 1436-1600 FROM N.A.

RX MEDLINE=99252212; PubMed=10233982;

RA Lee J.-S., Hartuna T., Ishimoto A., Honjo T., Yanagawa S.-I.;

RT "Intercisternal type A particle-mediated activation of the Notch4/int3

RT gene in a mouse mammary tumor: generation of truncated Notch4/int3

RT mRNAs by retroviral splicing events. ";

RL J. Virol. 73:5166-5171(1999).

LN [6]

RP FUNCTION.

RX MEDLINE=21244657; PubMed=11344305;

RA Uytendaele H., Ho J., Rossant J., Kitajewski J.;

RT "Vascular patterning defects associated with expression of activated

RT Notch4 in embryonic endothelium";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:5643-5648(2001).
 RP SEQUENCE OF 1463-1964, POST-TRANSLATIONAL PROCESSING, AND MUTAGENESIS
 OF VAL-1463.
 RA MEDLINE=21523956; PubMed=11518718;
 RA Saxena M.T., Schroeter E.H., Mumm U.S., Kopan R.;
 RT "Murine notch homologs (NI-4) undergo presenilin-dependent
 proteolysis.";
 RL J. Biol. Chem. 276:40268-40273(2001).
 RN (8)
 RP POST-TRANSLATIONAL PROCESSING.
 RA MEDLINE=21374376; PubMed=1459941;
 RA Mizutani T., Taniguchi Y., Aoki T., Hashimoto N., Honjo T.;
 RT "Conservation of the biochemical mechanisms of signal transduction
 among mammalian Notch family members";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9026-9031(2001).
 CC -1- FUNCTION: Functions as a receptor for membrane-bound ligands
 Jagged1, Jagged2 and Delta1 to regulate cell-fate determination.
 CC Upon ligand activation through the released notch intracellular
 domain (NICD) it forms a transcriptional activator complex with
 RBP-J kappa and activates genes of the enhancer of split locus.
 CC Affects the implementation of differentiation, proliferation and
 CC apoptotic programs (by similarity). May regulate branching
 CC morphogenesis in the developing vascular system.
 CC -1- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-
 CC terminal fragment N(EC) which are probably linked by disulfide
 CC bonds.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Following
 CC proteolytical processing NICD is translocated to the nucleus.
 CC -1- TISSUE SPECIFICITY: Highly expressed in lung, moderately in heart
 CC kidney, and at lower levels in the ovary and skeletal muscle. A
 CC very low expression is seen in the brain, intestine, liver and
 CC testis.
 CC -1- DEVELOPMENTAL STAGE: Highly expressed in endothelial cells during
 CC embryonic development from 9.0 dpc.
 CC -1- PTM: Synthesized in the endoplasmic reticulum as an inactive form
 CC which is proteolytically cleaved by a furin-like convertase in the
 CC trans-Golgi network before it reaches the plasma membrane to yield
 CC an active, ligand-accessible form. Cleavage results in a C-
 CC terminal fragment N(TM) and a N-terminal fragment N(EC). Following
 CC ligand binding, it is cleaved by TNF-alpha converting enzyme
 CC (TACE) to yield a membrane-associated intermediate fragment called
 CC notch extracellular truncation (NEXT). This fragment is then
 CC cleaved by presenilin dependent gamma-secretase to release a
 CC notch-derived peptide containing the intracellular domain (NICD)
 CC from the membrane.
 CC -1- PTM: Phosphorylated.
 CC -1- DISEASE: Loss of the extracellular domain causes constitutive
 CC activation of the Notch protein, which leads to hyperproliferation
 CC of glandular epithelial tissues and development of mammary
 CC carcinomas.
 CC -1- SIMILARITY: BELONGS TO THE NOTCH FAMILY.
 CC -1- SIMILARITY: Contains 29 EGF-like domains.
 CC -1- SIMILARITY: Contains 3 Lin/Notch repeats.
 CC -1- SIMILARITY: Contains 5 ANK repeats.
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
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 CC or send an email to license@sdb.ch).

DR PIR: T09059; T09059.
 DR HSGF; P08709; 1BP9.
 DR MGD; MGI:107471; Notch4.
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR000152; Asx hydroxyl.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR001438; EGF_1T.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR002049; LamInn_EGF.
 DR InterPro; IPR000800; Notch.
 DR Pfam; PF00023; ank; 6.
 DR Pfam; PF00008; EGF; 27.
 DR Pfam; PF00066; notch; 2.
 DR PRINTS; PR00010; EGFLOOD.
 DR PRINTS; PR00011; EGFAMININ.
 DR PRINTS; PR01452; NOTCH.
 DR SMART; SM00248; ANK; 6.
 DR SMART; SM00179; EGF_CA; 11.
 DR SMART; SM00004; NL; 2.
 DR PROSITE; PS50088; ANK_REPEAT; 5.
 DR PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 11.
 DR PROSITE; PS00022; EGF_1; 28.
 DR PROSITE; PS01186; EGF_2; 21.
 DR PROSITE; PS01187; EGF_CA; 9.
 KW Receptor; Transcription regulation; Activator; Differentiation;
 KW Developmental protein; Repeat; ANK repeat; EGF-like domain;
 KW Transmembrane; Glycoprotein; Signal; Phosphorylation; Proto-oncogene.
 FT SIGNAL 1
 FT CHAIN 21 1964
 FT CHAIN 1411 1964
 FT CHAIN 1428 1964
 FT CHAIN 1463 1964
 FT CHAIN 21 1443
 FT TRANSMEM 1444 1464
 FT DOMAIN 1465 1964
 FT DOMAIN 21 60
 FT DOMAIN 61 112
 FT DOMAIN 115 152
 FT DOMAIN 153 189
 FT DOMAIN 191 229
 FT DOMAIN 231 371
 FT DOMAIN 273 309
 FT DOMAIN 311 350
 FT DOMAIN 352 388
 FT DOMAIN 389 427
 FT DOMAIN 429 470
 FT DOMAIN 472 508
 FT DOMAIN 510 546
 FT DOMAIN 548 584
 FT DOMAIN 586 622
 FT DOMAIN 623 656
 FT DOMAIN 658 686
 FT DOMAIN 688 724
 FT DOMAIN 726 762
 FT DOMAIN 764 800
 FT DOMAIN 803 839
 FT DOMAIN 841 877
 FT DOMAIN 878 924
 FT DOMAIN 926 962
 FT DOMAIN 964 1000
 FT DOMAIN 1002 1040
 FT DOMAIN 1042 1081
 FT DOMAIN 1083 1122
 FT DOMAIN 1126 1167
 FT DOMAIN 1168 1208
 FT REPEAT 1209 1242
 FT REPEAT 1243 1282
 FT REPEAT 1283 1317
 FT REPEAT 1318 1357
 FT REPEAT 1358 1397
 FT REPEAT 1398 1437
 FT REPEAT 1438 1477
 FT REPEAT 1478 1517
 FT REPEAT 1518 1557
 FT REPEAT 1558 1597
 FT REPEAT 1598 1637
 FT REPEAT 1638 1677
 FT REPEAT 1678 1717
 FT REPEAT 1718 1757

Query Match 13.0%; Score 196; DB 1; Length 1964;
 Best Local Similarity 34.2%; Pred. No. 1,9e-07;
 Matches 50; Conservative 12; Mismatches 54; Indels 30; Gaps 7;

80 AARPRYACCPGK-RTSGLPAGCAAIQPPRRNGSGVQRP--RCRCPYGMKRDITQ 135
 134 ASGRPQCSCEPMTGBOCQRLRFCSA---NPNANGVGLIATYVPIQCRCPGFEHGTCE 189
 136 SVVDECSARRGGCPQ--RCINMAGSYWCOC---WEGHSLSADGTLCTP-----KGGPRVA 186
 190 RUIINEFLRPPDPCQCTSHNTLGSYQCLCPVGGBGPCKLRKAGACPPSPGCIANGTCCQLV 249
 187 PNP-----TGVDSAMKEK 199
 250 PEGHSFPHLCLCPGFTGLDCENNP 275

RESULT 2
 NTC4_HUMAN STANDARD; PRT; 2003 AA.
 AC Q99466; O00306; Q99458; Q9H358; Q9UI19; Q9UIJ0;
 ID 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neurogenic locus notch homolog protein 4 precursor (Notch 4) (hNotch4).
 GN NOTCH4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RP [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND POLYMORPHISM OF POLY-LEU.
 RC TISSUE=Placenta;
 RC MEDLINE=97311416; PubMed=9168133;
 RA Sugaya K., Sasauma S.-I., Nohata J., Kimura T., Fukagawa T., Nakamura Y., Ando A., Inoko H., Ikemura T., Mita K.;
 RA "Gene organization of human NOTCH4 and (CTG)n polymorphism in this human counterpart gene of mouse proto-oncogene Int3.";
 RL Genomics 51:45-58(1998).
 RN [3]
 RP SEQUENCE OF 1-503 FROM N.A., AND VARIANTS GLN-117 AND GLN-317.
 RA Miyagawa T., Tokunaga K., Hojoh H.;
 RT "Human notch4 gene variant.";
 RL Submitted (FEB-1999) to the EMBL/genbank/DBJ databases.
 RN [4]
 RP IDENTIFICATION OF LIGANDS.
 RX MEDLINE=99180765; PubMed=10079256;
 RA Gray G.E., Mann K.S., Mitsiadis E., Henrique D., Gargangiu M.-L., Banks A., Lelman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.;
 RA "Human ligands of the Notch receptor.";
 RL Am. J. Pathol. 154:785-794(1999).
 CC -!- FUNCTION: Functions as a receptor for membrane-bound ligands. Jagged1, Jagged2 and Delta1 to regulate cell-fate determination. Upon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with RBP-J kappa and activates genes of the enhancer of split locus. Affects the implementation of differentiation, proliferation and apoptotic programs. May regulate branching morphogenesis in the developing vasculature system (By similarity).
 CC -!- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-terminal fragment N(IEC) which are probably linked by disulfide bonds (By similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein. Following proteolytic processing NICD is translocated to the nucleus.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Comment=Alternative splicing. Named isoforms=3;
 CC isoforms;
 CC Comment=Experimental confirmation may be lacking for some isoforms;
 CC Name=1;
 CC IsoId=Q99466-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q99466-2; Sequence=VSP_001406;
 CC Name=3;
 CC IsoId=Q99466-3; Sequence=VSP_001407;
 CC TISSUE SPECIFICITY: Highly expressed in the heart, moderately in the lung and placenta and at low levels in the liver, skeletal muscle, kidney, pancreas, spleen, lymph node, thymus, bone marrow and fetal liver. No expression was seen in adult brain or peripheral blood leukocytes.
 CC -!- PTM: Synthesized in the endoplasmic reticulum as an inactive form which is proteolytically cleaved by a furin-like convertase in the trans-golgi network before it reaches the plasma membrane to yield an active, ligand-accessible form. Cleavage results in a C-terminal fragment N(TM) and a N-terminal fragment N(IEC). Following ligand binding, it is cleaved by TNF-alpha converting enzyme (TACE) to yield a membrane-associated intermediate fragment called notch extracellular truncation (NEXT). This fragment is then cleaved by presenilin dependent gamma-secretase to release a notch-derived peptide containing the intracellular domain (NICD) from the membrane (By similarity).
 CC -!- PTM: Phosphorylated (By similarity).
 CC -!- POLYMORPHISM: The poly-leu region of NOTCH4 (in the signal peptide) is polymorphic and the number of leu varies in the population (from 6 to 12).
 CC -!- SIMILARITY: BELONGS TO THE NOTCH FAMILY.
 CC -!- SIMILARITY: Contains 28 EGF-like domains.
 CC -!- SIMILARITY: Contains 3 Lin/Notch repeats.
 CC -!- SIMILARITY: Contains 5 ANK repeats.
 CC -!- CAUTION: Ref.1 sequence differs from that shown due to frameshifts in position 1438 to 1463.
 CC -----
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 CC -----
 CC EMBL; D63395; BAA09708.1; ALT_FRAME.
 DR EMBL; D86566; BAA13116.1; -;
 DR EMBL; U95399; AAC32288.1; -;
 DR EMBL; U89335; AAC63097.1; -;
 DR EMBL; AB023964; BAB20317.1; -;
 DR EMBL; AB024520; BAA88951.1; -;
 DR EMBL; AB024578; BAA88952.1; -;
 DR HSSP; P08709; IBR9.
 DR HSSP; HGNC:7884; NOTCH4.
 DR MIM; 164951; -;
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR000152; Asx_hydroxy1.
 DR InterPro; IPR000742; EGF 2.
 DR InterPro; IPR001481; EGF Ca.
 DR InterPro; IPR001438; EGF II.
 DR InterPro; IPR006209; EGF II.
 DR InterPro; IPR002049; Laminin_EGF.
 DR InterPro; IPR000800; Notch.
 DR Pfam; PF00066; notch; 2.
 DR Pfam; PF00008; EGF; 26.
 DR Pfam; PF00023; ank; 6.
 DR PRINTS; PR00010; EGFBL00D.
 DR PRINTS; PR00011; EGFBL00N.
 DR PRINTS; PR01452; NOTCH.
 DR SMART; SM00248; ANK; 5.
 DR SMART; SM00179; EGF_CA; 11.

DR SMART, SM00004; NL; 3.
 DR PROSITE; PSS0088; ANK_REPEAT: 5.
 DR PROSITE; PSS0297; ANK_REPEAT_REGION: 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 11.
 DR PROSITE; PS00022; EGF_1; 28.
 DR PROSITE; PS01186; EGF_2; 21.
 DR PROSITE; PS01187; EGF_CA; 9.
 KW Receptor; Transcription regulation; Activator; Differentiation;
 KW Developmental protein; Repeat; ANK repeat; EGF-like domain;
 KW Transmembrane; Glycoprotein; Signal; Phosphorylation; Polymorphism;
 KW Triple repeat expansion; Alternative splicing.
 FT CHAIN 1 23
 FT CHAIN 24 2003
 FT CHAIN 1432 2003
 FT CHAIN 1467 2003
 FT DOMAIN 24 1447
 FT TRANSEM 1448 1468
 FT DOMAIN 1469 2003
 FT DOMAIN 24 63
 FT DOMAIN 64 115
 FT DOMAIN 118 155
 FT DOMAIN 156 192
 FT DOMAIN 194 232
 FT DOMAIN 234 274
 FT DOMAIN 276 312
 FT DOMAIN 314 353
 FT DOMAIN 355 391
 FT DOMAIN 392 430
 FT DOMAIN 432 473
 FT DOMAIN 475 511
 FT DOMAIN 513 549
 FT DOMAIN 551 587
 FT DOMAIN 589 625
 FT DOMAIN 626 658
 FT DOMAIN 661 689
 FT DOMAIN 691 727
 FT DOMAIN 729 765
 FT DOMAIN 767 803
 FT DOMAIN 806 842
 FT DOMAIN 844 880
 FT DOMAIN 882 928
 FT DOMAIN 930 966
 FT DOMAIN 968 1004
 FT DOMAIN 1006 1044
 FT DOMAIN 1046 1085
 FT DOMAIN 1087 1126
 FT DOMAIN 1130 1171
 FT DOMAIN 1172 1476
 FT DOMAIN 1475 1212
 FT REPEAT 1213 1246
 FT REPEAT 1247 1286
 FT REPEAT 1286 1633
 FT REPEAT 1633 1665
 FT REPEAT 1666 1698
 FT REPEAT 1700 1732
 FT REPEAT 1733 1765
 FT REPEAT 1766 1798
 FT REPEAT 1798 28
 FT DISULFID 28 51
 FT DISULFID 53 62
 FT DISULFID 68 80
 FT DISULFID 74 103
 FT DISULFID 105 114
 FT DISULFID 122 133
 FT DISULFID 137 143
 FT DISULFID 145 154
 FT DISULFID 160 171
 FT DISULFID 180 180
 FT DISULFID 182 191
 FT DISULFID 198 211
 FT DISULFID 205 230
 FT DISULFID 231 231

FT -DISULFID 238 249 BY SIMILARITY.
 Query Match 12.5%; Score 188.5; DB 1; Length 2003;
 Best Local Similarity 29.6%; Pred. No. 7,4e-07;
 Matches 61; Conservative 17; Mismatches 87; Indels 41; Gaps 11;
 QY 80 APARPRVACCPGK-RTSGLGACGAATCQPPRRGGSCVQPG---RCRCPAGMRGDTQC 135
 DB 137 ASGRQCCCMRMTGECQQLDFGSA---NPCVNGVCLMRYFOIQCHCPGFGHACE 192
 QY 136 SDVDECSARRGGCPQ--RCINTAGSYWCQWEGHSLADGTLVCPKGG--PPRYAVNPTG 191
 DB 193 RVNHCFOQPPGCPKGTSCNHTLGSFQCLCPVQQ---EGPRCELRAQPCPPGGSN--CG 247
 QY 192 VDSAMKEVQRLQSRVLDLLEKQLVLAPLHSLSAQALRHLPD---PSSLVHSFQQL 247
 DB 248 TCQLMPEK-----DSTFHLCLCPGFRIG-----PCEVNPDMCVSHQCCNG 288
 QY 248 GRI-DSLSEQISFLEQLGSCSKKD 272
 DB 289 GTCQDGLDLYTCLCPETWTGMDCESD 314
 RESULT 3
 NEI2 MOUSE STANDARD; PRT; 816 AA.
 AC Q612Z0;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein kinase C-binding protein NEI2 precursor (NEI-1like protein 2) (MEI91 protein).
 GN NEI2 OR MEI91.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Eikins D.A., Rossi J.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RT [2]
 RS TSP N-TERMINAL DOMAIN.
 RP MEDLINE=98153258; PubMed=9480764;
 RA Beckmann G., Hanke J., Bork P., Reich J.;
 RT "Merging extracellular domains: fold prediction for laminin G-like and amino-terminal thrombospondin-like modules based on homology to pentraxins.";
 RL J. Mol. Biol. 275:725-730(1998).
 CC -1- SUBCELLULAR LOCATION: Secreted (By similarity).
 CC -1- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
 CC -1- SIMILARITY: Contains 5 WFC domains.
 CC -1- SIMILARITY: Contains 6 EGF-like domains.
 CC -----
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 CC -----
 CC EMBL; U59230; AAB02924.1; ALT_INT.
 CC HSSP; P00740; IEDM.
 DR MED; MGI:1856510; Nel12.
 DR InterPro; IPR000152; Asx_hydroxy1.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_Like.
 DR InterPro; IPR001791; Laminin_G.
 DR InterPro; IPR001129; TSPN.
 DR InterPro; IPR001007; WVF_C.
 DR Pfam; PF00006; EGF_5.
 DR Pfam; PF02210; TSPN_1.

DR Pfam: PF00093; vwc; 2.
 DR SMART; SM00179; EGF CA; 3.
 DR SMART; SM00282; Lamg; 1.
 DR SMART; SM00210; TSPN; 1.
 DR SMART; SM00214; vwc; 2.
 DR PROSITE; PS00010; ASK_HYDROXYL; 3.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS01187; EGF CA; 3.
 DR PROSITE; PS01208; vwc; 1; 2.
 DR PROSITE; PS00184; vwc; 2; 2.
 KM Glycoprotein; EGF-like domain; Repeat; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 816
 FT DOMAIN 30 258
 FT DOMAIN 272 331
 FT DOMAIN 332 396
 FT DOMAIN 377 439
 FT DOMAIN 440 481
 FT DOMAIN 482 522
 FT DOMAIN 521 553
 FT DOMAIN 555 601
 FT DOMAIN 602 637
 FT DOMAIN 638 693
 FT DOMAIN 698 756
 FT DOMAIN 758 813
 FT DOMAIN 813 401
 FT DISULFID 407 422
 FT DISULFID 424 438
 FT DISULFID 444 457
 FT DISULFID 451 466
 FT DISULFID 468 480
 FT DISULFID 486 499
 FT DISULFID 493 508
 FT DISULFID 510 521
 FT DISULFID 525 535
 FT DISULFID 529 541
 FT DISULFID 543 552
 FT DISULFID 559 572
 FT DISULFID 566 581
 FT DISULFID 583 600
 FT DISULFID 606 619
 FT DISULFID 613 628
 FT DISULFID 630 636
 FT CARBOHYD 53 53
 FT CARBOHYD 225 225
 FT CARBOHYD 293 293
 FT CARBOHYD 298 298
 FT CARBOHYD 517 517
 FT CARBOHYD 615 615
 FT CARBOHYD 635 635
 SQ SEQUENCE 816 AA; 91163 MW; 58BD0A946887E74D CRC64;

Query Match 12.3%; Score 185; DB 1; Length 816;
 Beel Local Similarity 29.4%; Pred. No. 5.4e-07;
 Matches 47; Conservative 21; Mismatches 64; Indels 28; Gaps 7;

Oy 26 RGRVCAVRAHGDPIVSESEFVQRYVPLTT--CGHRAACSTRTTYTAARRSGLAPA 82
 Db 461 RGSFVCKVKT-GYTRIDYVSCHEBCLTTHNCCENMLC--FNTV-----G 504
 Oy 83 RPRVACCGMWRKTSGLPACAGALICOPPCRRNGGSCVOPGRGRCPPAGWRGDRTCQSPDVDCS 142
 Db 505 GHNCVCKRKYTYGN----GTTCKAFKDCGRNGAGALIANVCAACPGGFGPSCETDIDECSS 560
 Oy 143 ARRGCCPQR--CINTAGSYWCCMEGHSLSADGTLCPVKG 180
 Db 561 EGFVQCCDRANCLINLPGVYHGCRDGYH---DNGMFAFGG 597

RESULT 4
 FBZ_MOUSE STANDARD; PRT; 2907 AA.
 ID FBZ_MOUSE

AC O61555; O63957; 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Fibrillin 2 precursor.
 GN FBZ2 OR FBZ-2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid:10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95263670; PubMed=7744963;
 RA Zhang H., Hu W., Ramirez F.;
 RT "Developmental expression of fibrillin genes suggests heterogeneity
 of extracellular microfibrils";
 RL J. Cell Biol. 129:1165-1176(1995).
 RN [2]
 RP SEQUENCE OF 210-317 FROM N.A.
 RX MEDLINE=94140368; PubMed=8307578;
 RA Francke U., Pereira L., Zhang H., Sanguinetti C., Ramirez F., Bonadio J.,
 RT "Fibrillin genes map to regions of conserved mouse/human synteny on
 mouse chromosomes 2 and 18";
 RL Genomics 18:667-672(1993).
 CC -I- FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS
 THAT BINDS CALCIUM. FIBRILLIN-1-CONTAINING MICROFIBRILS PROVIDE
 LONG-TERM FORCE BEARING STRUCTURAL SUPPORT.
 CC -I- SIMILARITY: Contains 7 TGF-beta binding protein (TGFbeta) domains.
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; L39790; AAA74908.1; -
 DR EMBL; S69359; AAC60685.1; -
 DR PIR; A57278; A57278.
 DR HSSP; P35555; IEMN.
 DR MGD; MGI:95490; Fbn2.
 DR GO: GO:0030326; P: limb morphogenesis; IMP.
 DR InterPro; IPR000152; Ask_Hydroxyl.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR001438; EGF_1.
 DR InterPro; IPR006209; EGF_Like.
 DR InterPro; IPR002212; Fibril-assoc.
 DR Pfam; PF00008; EGF; 45.
 DR Pfam; PF00683; TB; 9.
 DR PRINTS; PR00010; EGFBL00D.
 DR SMART; SM00179; EGF CA; 43.
 DR PROSITE; PS00010; ASX_HYDROXYL; 43.
 DR PROSITE; PS00022; EGF_1; 2.
 DR PROSITE; PS01186; EGF_2; 36.
 DR PROSITE; PS01187; EGF_CA; 43.
 KW Extracellular matrix; Calcium-binding; Glycoprotein; EGF-like domain;
 KW Repeat; Signal; Multigene family.
 FT SIGNAL 1 28
 FT CHAIN 29 2907
 FT DOMAIN 111 142
 FT DOMAIN 145 176
 FT DOMAIN 176 208
 FT DOMAIN 216 317
 FT DOMAIN 318 359
 FT DOMAIN 360 426
 FT REPEAT 360 426
 FT DOMAIN 487 527
 FT DOMAIN 528 567
 FT DOMAIN 568 609
 FT DOMAIN 610 650
 FT DOMAIN 651 691
 FT FIBRILLIN 2.
 FT EGF-LIKE 1.
 FT EGF-LIKE 2.
 FT EGF-LIKE 3.
 FT EGF-LIKE 4.
 FT EGF-LIKE 5.
 FT TGFBR 1.
 FT EGF-LIKE 6.
 FT EGF-LIKE 7.
 FT EGF-LIKE 8.
 FT EGF-LIKE 9.
 FT EGF-LIKE 10.

FT	REPEAT	692	760	TGRBP 2.
FT	DOMAIN	761	802	EGF-LIKE 11, CALCITUM-BINDING.
FT	DOMAIN	803	844	EGF-LIKE 12, CALCITUM-BINDING.
FT	DOMAIN	845	883	EGF-LIKE 13, CALCITUM-BINDING.
FT	DOMAIN	948	989	EGF-LIKE 14, CALCITUM-BINDING.
FT	REPEAT	990	1065	TGRBP 3.
FT	DOMAIN	1066	1107	EGF-LIKE 15, CALCITUM-BINDING.
FT	DOMAIN	1108	1150	EGF-LIKE 16, CALCITUM-BINDING.
FT	DOMAIN	1151	1192	EGF-LIKE 17, CALCITUM-BINDING.
FT	DOMAIN	1193	1234	EGF-LIKE 18, CALCITUM-BINDING.
FT	DOMAIN	1235	1275	EGF-LIKE 19, CALCITUM-BINDING.
FT	DOMAIN	1276	1317	EGF-LIKE 20, CALCITUM-BINDING.
FT	DOMAIN	1318	1359	EGF-LIKE 21, CALCITUM-BINDING.
FT	DOMAIN	1360	1400	EGF-LIKE 22, CALCITUM-BINDING.
FT	DOMAIN	1401	1441	EGF-LIKE 23, CALCITUM-BINDING.
FT	DOMAIN	1442	1483	EGF-LIKE 24, CALCITUM-BINDING.
FT	DOMAIN	1484	1524	EGF-LIKE 25, CALCITUM-BINDING.
FT	REPEAT	1525	1565	EGF-LIKE 26, CALCITUM-BINDING.
FT	DOMAIN	1566	1642	TGRBP 4.
FT	DOMAIN	1643	1684	EGF-LIKE 27, CALCITUM-BINDING.
FT	DOMAIN	1685	1726	EGF-LIKE 28, CALCITUM-BINDING.
FT	REPEAT	1727	1800	TGRBP 5.
FT	DOMAIN	1801	1842	EGF-LIKE 29, CALCITUM-BINDING.
FT	DOMAIN	1843	1884	EGF-LIKE 30, CALCITUM-BINDING.
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FT	DOMAIN	1966	2008	EGF-LIKE 33, CALCITUM-BINDING.
FT	DOMAIN	2009	2048	EGF-LIKE 34, CALCITUM-BINDING.
FT	DOMAIN	2049	2090	EGF-LIKE 35, CALCITUM-BINDING.
FT	REPEAT	2091	2163	TGRBP 6.
FT	DOMAIN	2164	2205	EGF-LIKE 36, CALCITUM-BINDING.
FT	DOMAIN	2206	2245	EGF-LIKE 37, CALCITUM-BINDING.
FT	DOMAIN	2246	2286	EGF-LIKE 38, CALCITUM-BINDING.
FT	DOMAIN	2287	2330	EGF-LIKE 39, CALCITUM-BINDING.
FT	DOMAIN	2331	2372	EGF-LIKE 40, CALCITUM-BINDING.
FT	REPEAT	2373	2441	TGRBP 7.
FT	DOMAIN	2442	2483	EGF-LIKE 41, CALCITUM-BINDING.
FT	DOMAIN	2484	2524	EGF-LIKE 42, CALCITUM-BINDING.
FT	DOMAIN	2525	2563	EGF-LIKE 43, CALCITUM-BINDING.
FT	DOMAIN	2564	2606	EGF-LIKE 44, CALCITUM-BINDING.
FT	DOMAIN	2607	2646	EGF-LIKE 45, CALCITUM-BINDING.
FT	DOMAIN	2647	2687	EGF-LIKE 46, CALCITUM-BINDING.
FT	DOMAIN	2688	2727	EGF-LIKE 47, CALCITUM-BINDING.
FT	DISULFID	115	124	BY SIMILARITY.
FT	DISULFID	119	130	BY SIMILARITY.
FT	DISULFID	132	141	BY SIMILARITY.
FT	DISULFID	149	159	BY SIMILARITY.
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FT	DISULFID	180	190	BY SIMILARITY.
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FT	DISULFID	772	786	BY SIMILARITY.
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FT	DISULFID	814	828	BY SIMILARITY.
FT	DISULFID	830	843	BY SIMILARITY.
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FT	DISULFID	1261	1274	BY SIMILARITY.
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FT	DISULFID	1453	1467	BY SIMILARITY.
FT	DISULFID	1469	1482	BY SIMILARITY.
FT	DISULFID	1488	1499	BY SIMILARITY.
FT	DISULFID	1494	1508	BY SIMILARITY.
FT	DISULFID	1510	1523	BY SIMILARITY.
FT	DISULFID	1529	1540	BY SIMILARITY.
FT	DISULFID	1535	1549	BY SIMILARITY.
FT	DISULFID	1551	1564	BY SIMILARITY.
FT	DISULFID	1647	1659	BY SIMILARITY.
FT	DISULFID	1654	1668	BY SIMILARITY.
FT	DISULFID	1670	1683	BY SIMILARITY.
FT	DISULFID	1689	1701	BY SIMILARITY.
FT	DISULFID	1696	1710	BY SIMILARITY.

Query Match 12.2%; Score 183.5; DB 1; Length 2907;
Best Local Similarity 23.9%; Pred. No. 2.7e-06;
Matches 60; Conservative 19; Mismatches 85; Indels 87; Gaps 7;

QY	2	RGSGVLLMMLVLAAGTETAY-----RPRGRVCAVRAHAGPVSSESPFYQRYVQPLT 54
Db	77	RGQDILRG--PNVCGSRFHSYCCPGWKTLPGANQCTVPICRNSCGDGFCSR--PVMC 130
QY	55	TCDDHRAACST--YRITRYTAVRSPFLAPARPRVACCPGMRRTGLPACGAALICQPPCR 112
Db	131	TCSSQIISPTLGRKRSIQCCSVRCMNGGICADHDQCKQKGYIGT-----YCGQPVICENCCQ 185
QY	113	NGGSCVQDPRRCRCPAGWRGDTCC----- 135
Db	186	NGRGRICGNRACAVYGFTRGQCEBRYRTPCFQVNNNMCCGQLTGIVCTKTLCCATIGR 245
QY	136	-----SVDKCSARRGCP-QRCINTMGSYWCQWE 165
Db	246	AMGHECENCPAQPPCRPGRPIINIRTGACQDVDECOALPGLCGGANCTINTVGSFRCRCPA 305

OY 166 GHSLSDGTLG 176
DB 306 GHKQSEFTQKC 316

RESULT 5
NEL2_HUMAN STANDARD; PRT; 816 AA.
ID NEL2_HUMAN
AC O99435:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein kinase C-binding protein NEL2 precursor (NEL-like protein 2)
DE (Ne1-related protein 2).
GN NEL2 OR NRP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97131504; PubMed=8975702;
RA Watanabe T.K., Katagiri T., Suzuki M., Shimizu F., Fujiwara T.,
RA Kanemoto N., Nakamura Y., Hirai Y., Maekawa H., Takahashi E.;
RT "Cloning and characterization of two novel human cDNAs (NEL1 and
RT NEL2) encoding proteins with six EGF-like repeats.";
RT Genomics 38:273-276(1996).
RN [2]
RP TSP N-TERMINAL DOMAIN.
RX MEDLINE=98153258; PubMed=9480764;
RA Beckmann G., Hanke J., Bork P., Reich J.;
RT "Merging extracellular domains: fold prediction for laminin G-like
RT and amino-terminal thrombospondin-like modules based on homology to
RT pentraxins.";
RT J. Mol. Biol. 275:725-730(1998).
CC -1- SUBUNIT: HOMOTRIMER. BINDS TO PKC BETA-1 (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Secreted (By similarity) domain.
CC -1- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
CC -1- SIMILARITY: Contains 5 WFC domains.
CC -1- SIMILARITY: Contains 6 EGF-like domains.
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CC or send an email to license@isb-stb.ch).

DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 4.
DR PROSITE; PS01187; EGF_CA; 3.
DR PROSITE; PS01208; WFC_1; 2.
DR PROSITE; PS0184; WFC_2; 3.
DR PROSITE; PS0184; WFC_3; 3.
KW Glycoprotein; EGF-like domain; Repeat; Signal.
FT SIGNAL 1 24
FT CHAIN 25 816
FT DOMAIN 30 258
FT DOMAIN 272 331
FT DOMAIN 332 396
FT DOMAIN 397 439
FT DOMAIN 440 481
FT DOMAIN 482 522
FT DOMAIN 521 553
FT DOMAIN 555 601
FT DOMAIN 602 637
FT DOMAIN 638 693
FT DOMAIN 698 756
FT DOMAIN 758 813
FT DISULFID 401 413
FT DISULFID 407 422
FT DISULFID 424 438
FT DISULFID 444 457
FT DISULFID 451 466
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FT DISULFID 583 600
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FT DISULFID 613 628
FT DISULFID 630 636
FT CARBOHYD 53 53
FT CARBOHYD 225 225
FT CARBOHYD 293 293
FT CARBOHYD 298 298
FT CARBOHYD 517 517
FT CARBOHYD 615 615
FT CARBOHYD 635 635
SQ SEQUENCE 816 AA; 91346 MW; 89370B987DC7A324 CRC64;
Query Match 12.1%; Score 182.5; DB 1; Length 816;
Best Local Similarity 37.9%; Pred. No. 8.5e-07;
Matches 36; Conservative 13; Mismatches 37; Indels 9; Gaps 3;
OY 88 CCEGKRTSGLPAGCAALICQPPCRNGSSCVQPGRCRCPAGWRGPTCCSDVDEGARRGG 147
DB 510 CKPGYTGNN---GTTCKKAFCKDGRNGGACIAANVACACPGFTGSCETDIDECSDGFVQ 565
OY 148 CPQR--CINTAGSYWVCCQMEGHSSUSADGTLCPVKG 180
DB 566 CDSRANCLNLPQWYHCBRDGTH--DNQMFSPSG 597
RESULT 6
NEL1_HUMAN STANDARD; PRT; 810 AA.
ID NEL1_HUMAN
AC O92832; Q9Y472;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Protein kinase C-binding protein NEL1 precursor (NEL-like protein 1)
DE (Ne1-related protein 1).
GN NEL1 OR NRP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=97131504; PubMed=8975702;
 RA Watanabe T.K., Katagiri T., Suzuki M., Shimizu F., Fujiwara T.,
 RA Kanemoto N., Nakamura Y., Hirai Y., Maekawa H., Takahashi E.;
 RT "Cloning and characterization of two novel human cDNAs (NEHL1 and
 RL NEHL2) encoding proteins with six EGF-like repeats.";
 RL Genomics 38:273-276(1996).
 RN [2]
 RP SEQUENCE OF 383-810 FROM N.A.
 RA Ting K., Vaetardis H., Mulliken J.B., Bertolami C., Wen Z.,
 RA Young M., Tieu A., Kwong E.;
 RL "nel1 homolog gene expression in craniofacial anomalies.";
 RT Submitted (Sep-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBUNIT: HOMOTRIMER. BINDS TO PKC BETA-1 (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCALIZATION: Secreted (By similarity).
 CC -1- DISEASE: EXPRESSED IN CRANIOFACIAL ANOMALIES.
 CC -1- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
 CC -1- SIMILARITY: Contains 5 WFC domains.
 CC -1- SIMILARITY: Contains 6 EGF-like domains.
 CC -1- CAUTION: REP.2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS
 IN POSITIONS 427 AND 771.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; D93017; BAAL1680.1; -; -;
 DR EMBL; U57523; AAB06946.1; ALT_FRAME.
 DR HSSP; P07204; IADX.
 DR GeneW; HGNC:7750; NEHL1.
 DR MIM; 602319; -;
 DR GO; GO:0007399; P-neurogenesis; TAS.
 DR InterPro; IPR000152; ASX_hydroxyl.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_Like.
 DR InterPro; IPR001791; Laminin_G.
 DR InterPro; IPR003129; TSPN.
 DR Pfam; PR000008; EGF_5.
 DR Pfam; PF02210; TSPN; 1.
 DR Pfam; PR00093; wfc; 2.
 DR SMART; SM00179; EGF_CA; 2.
 DR SMART; SM00282; LamG; 1.
 DR SMART; SM00210; TSPN; 1.
 DR SMART; SM00214; VWC_3.
 DR PROSITE; PS00010; ASX_HYDROXYL; 3.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 3.
 DR PROSITE; PS01187; EGF_CA; 3.
 DR PROSITE; PS01208; WFC_1; 2.
 DR PROSITE; PS01284; WFC_2; 2.
 KM Glycoprotein; EGF-like domain; Repeat; Signal.
 FT SIGNAL 1 16
 FT CHAIN 17 810
 FT DOMAIN 81 230
 FT DOMAIN 271 332
 FT DOMAIN 335 390
 FT DOMAIN 391 433
 FT DOMAIN 434 475
 FT DOMAIN 476 516
 FT DOMAIN 515 547
 FT DOMAIN 549 595
 FT DOMAIN 596 631
 FT DOMAIN 632 687
 FT DOMAIN 692 750
 FT DOMAIN 752 807

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 FT DISULFID 401 416 BY SIMILARITY.
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 FT DISULFID 577 594 BY SIMILARITY.
 FT DISULFID 600 613 BY SIMILARITY.
 FT DISULFID 607 622 BY SIMILARITY.
 FT DISULFID 624 630 BY SIMILARITY.
 FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 224 224 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 372 372 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 511 511 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 562 562 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 708 708 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 722 732 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 758 758 N-> D (IN REF. 2).
 FT CONFLICT 383 383 N-> H (IN REF. 2).
 FT CONFLICT 573 573 Y-> C (IN REF. 2).
 FT CONFLICT 626 626 S-> C (IN REF. 2).
 SQ SEQUENCE 810 AA; 89606 MW; 549465E3A3F7AE8D0 CRC64;
 Query Match 12.1%; Score 182; DB 1; Length 810;
 Best Local Similarity 37.5%; Pred. No. 9.2e-07;
 Matches 36; Conservative 12; Mismatches 38; Indels 10; Gaps 3;
 QY 88 CCRGKWRKRTSGLPAGAGAAICQPPCGNNGSCQPGRCRCPAGMRGDTGCSQDVEGSRARGG 147
 DB 504 CKPQGVGN---GTCRAPFCEGGCRYYGTYCAVANKVCPSPSGFTGSHCKRDIDCESEGIIE 559
 QY 148 C--PORCINTAGSYWCQCQCEGH---SLSADGTLCV 177
 DB 560 CHNHSRCVNIPLPGWYHCECRSGRHHDDGTYSLGSESCI 595
 RESULT 7
 NEHL2 RAT STANDARD; PRT; 816 AA.
 AC O62918;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein kinase C-binding protein NEHL2 precursor (NEHL-like protein 2).
 GN NEHL2 OR NEL.
 OS Nattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=101116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RA MEDLINE=20017976; PubMed=10548494;
 RA Kuroda S., Oyasu M., Kawakami M., Kanayama N., Tanizawa K., Saito N.,
 RA Abe T., Matsunashi S., Ting K.;
 RT "Biochemical characterization and expression analysis of neural
 RL thrombospondin-1-like proteins NEHL1 and NEHL2.";
 RN Biochem. Biophys. Res. Commun. 265:79-86(1999).
 RP [2]
 RP TSP N-TERMINAL DOMAIN.
 RX MEDLINE=98153258; PubMed=9480764;

RA Beckmann G., Hanke J., Bork P., Reich J.,
 RT "Meying extracellular domains: fold prediction for laminin G-like
 RT and amino-terminal chondrospondin-like modules based on homology to
 RT pentraxins.";
 RL J. Mol. Biol. 275:725-730(1998).
 CC -1- SUBUNIT: HOMOTRIMER. BINDS TO PKC BETA-1.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
 CC -1- SIMILARITY: Contains 5 WFPC domains.
 CC -1- SIMILARITY: Contains 6 EGF-like domains.
 CC -----
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 CC EMBL; U48245; AAC72245.1; -
 CC HSSP; P00740; IEDM.
 DR InterPro: IPR000152; Asx hydroxyl.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR006209; EGF_Like.
 DR InterPro: IPR001791; Laminin_G.
 DR InterPro: IPR003129; TSPN.
 DR InterPro: IPR001007; VWF_C.
 DR Pfam; PR00008; EGF; 5.
 DR Pfam; PR02210; TSPN; 1.
 DR Pfam; PR00093; WVC; 3.
 DR SMART; SM00179; EGF_CA; 3.
 DR SMART; SM00282; LamG; 1.
 DR SMART; SM00210; TSPN; 1.
 DR SMART; SM00214; WVC; 3.
 DR PROSITE; PS00010; ASK_HYDROXYL; 3.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 4.
 DR PROSITE; PS01187; EGF_CA; 3.
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 FT 397 439 WVC 2.
 FT 440 481 EGF-LIKE 1.
 FT 482 522 EGF-LIKE 2.
 FT 523 553 EGF-LIKE 3.
 FT 554 601 EGF-LIKE 4.
 FT 602 637 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
 FT 638 698 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
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FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 FT CARBOHYD 517 517 N-LINKED (GLCNAC. . .) (POTENTIAL).
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 Db 510 CKRYTGN----GTTCKAFKRCGCKNGACGACIAANVACAPQGFRTGSCETDIDECSEBGFVQ 565
 QY 148 GPR--CINTAGSYWCQCMEGHSLSADGTLVCPK 180
 Db 566 CDSRANCIPLPGWYHCECRDGVH--DNGMFAPGG 597
 RESULT 8
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 AC 062919;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Protein kinase C-binding protein NEIL1 precursor (NEIL-like protein 1).
 OS Rattus norvegicus (Rat).
 GN NEIL1.
 ON Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Brain;
 RX MEDLINE=20017976; PubMed=10548494;
 RA Kuroda S., Oyasu M., Kakami M., Kanayama N., Tanizawa K., Saito N.,
 RA Abe T., Matsunashi S., Ting K.;
 RT "Biochemical characterization and expression analysis of neural
 RT chondrospondin-1-like proteins NEIL1 and NEIL2.";
 RL Biochem. Biophys. Res. Commun. 265:79-86(1999).
 CC -1- SUBUNIT: HOMOTRIMER. BINDS TO PKC BETA-1.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
 CC -1- SIMILARITY: Contains 5 WFPC domains.
 CC -1- SIMILARITY: Contains 6 EGF-like domains.
 CC -----
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 CC -----
 CC EMBL; U48246; AAC72252.1; -
 CC HSSP; P10756; T10756.
 DR InterPro: IPR000152; Asx hydroxyl.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR006209; EGF_Like.
 DR InterPro: IPR001791; Laminin_G.
 DR InterPro: IPR003129; TSPN.
 DR InterPro: IPR001007; VWF_C.
 DR Pfam; PR00008; EGF; 5.
 DR Pfam; PR02210; TSPN; 1.
 DR Pfam; PR00093; WVC; 2.
 DR SMART; SM00179; EGF_CA; 2.
 DR SMART; SM00282; LamG; 1.
 DR SMART; SM00210; TSPN; 1.

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DR SMART; SM00214; VWC; 2.
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FT SIGNAL 1
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FT DOMAIN 476 516
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Query Match 12.0%; Score 180; DB 1; Length 810;
Best Local Similarity 36.5%; Pred. No. 1.3e-06;
Matches 35; Conservative 13; Mismatches 38; Indels 10; Gaps 3;

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GN NEL.
OS Gallus gallus (Chicken).
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OC Archosauromorpha; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
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RP SEQUENCE FROM N.A.
RC TISSUE=Embryo.
RX MEDLINE=95383734; PubMed=7655083;
RA Matubashi S., Noji S., Koyama E., Myokai F., Ohuchi H.,
RA Taniguchi S., Hori K.;
RT "New gene, nel, encoding a Mr(93 k protein with EGF-like repeats is
RL strongly expressed in neural tissues of early stage chick embryos.";
RN Dev. Dyn. 203:212-222 (1995).
RN [2]
RP TSP N-TERMINAL DOMAIN.
RX MEDLINE=98153258; PubMed=9480764;
RA Beckmann G., Hanke J., Bork P., Reich J.;
RT "Merging extracellular domains: fold prediction for laminin G-like
RT and amino-terminal thrombospondin-like modules based on homology to
RT pentraxins.";
RL J. Mol. Biol. 275:725-730(1998).
CC -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN EARLY EMBRYONIC NEURAL
CC TISSUES (BRAIN, SPINAL CORD, DORSAL ROOT GANGLIA); LESS IN OTHER
CC TISSUES SUCH AS CELLS AROUND CARTILAGE, MYOCARDIUM, LUNG
CC MESONEPHRAL CELLS AND LIVER. AFTER HATCHING EXPRESSION IS
CC RESTRICTED TO NEURAL TISSUES INCLUDING RETINA.
CC -1- SIMILARITY: Contains 1 TSP N-terminal (TSPN) domain.
CC -1- SIMILARITY: Contains 5 WFPC domains.
CC -1- SIMILARITY: Contains 6 EGF-like domains.
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CC or send an email to license@sib-sib.ch).
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DR EMBL; D86747; BAA13167.1; -.
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DR InterPro; IPR000152; Asx hydroxyl.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR003129; TSPN.
DR Pfam; PF00008; EGF_5.
DR Pfam; PF02210; TSPN; 1.
DR Pfam; PF00093; VWC; 3.
DR SMART; SM00179; EGF_CA; 2.
DR SMART; SM00282; LamG; 1.
DR SMART; SM00210; TSPN; 1.
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DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 1.
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DR PROSITE; PS01187; EGF_CA; 3.
DR PROSITE; PS01208; WFPC_1; 2.
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KW Glycoprotein; EGF-like domain; Repeat; Signal.
FT SIGNAL 1 24
FT CHAIN 1 25
FT DOMAIN 30 816
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 DB 518 GTVCKAFCKDGGCRNCGACIASVWCACPOGFGTSPSCETDIDECSDGDFVQCDSPRANCIINLPG 577
 OY 158 SYWCQCWEGHSLADDTLCLVPRK 180
 DB 578 WYHCRCRDRGYH--DNGMPSBPG 597

RESULT 10
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 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Fibrillin 1 precursor.
 GN FBN1 OR FBN.
 OS Homo sapiens (Human).
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 RC TISSUE=Placenta; PubMed=8364578;
 RC MEDLINE=93372860;
 RA Pereira L.V., D'Alessio M., Ramirez F., Lynch J.R., Sykes B.,
 RA Pangilinan T., Bonadio J.;
 RT "Genomic organization of the sequence coding for fibrillin, the
 RT defective gene product in Marfan syndrome.";
 RL Hum. Mol. Genet. 2:961-968(1993).
 RN [2]
 RP SEQUENCE OF 1-932 FROM N.A.
 RC TISSUE=Fibroblast, and Placenta;
 RC MEDLINE=94010947; PubMed=7691719;
 RA Corson G.M., Chalberg S.C., Dietz H.C., Charbonneau N.L., Sakai L.Y.,
 RA "Fibrillin binds calcium and is coded by cDNAs that reveal a
 RT multidomain structure and alternatively spliced exons at the 5'
 RT end.";

RL Genomics 17:476-484(1993).
 RN [3]
 RP SEQUENCE OF 899-2871 FROM N.A.
 RA MEDLINE=91304568; PubMed=1852207;
 RA Maslen C.L., Corson G.M., Maddox B.K., Glanville R.W., Sakai L.Y.;
 RT "Partial sequence of a candidate gene for the Marfan syndrome.";
 RL Nature 352:334-337(1991).
 RN [4]
 RP SEQUENCE OF 813-1313 FROM N.A.
 RA MEDLINE=91304567; PubMed=1852206;
 RA Lee B., Godfrey M., Vitale E., Hori H., Mattei M.-G., Sarfarazi M.,
 RA Tsbouras P., Ramirez F., Hollister D.W.;
 RT "Linkage of Marfan syndrome and a phenotypically related disorder to
 RT two different fibrillin genes.";
 RL Nature 352:330-334(1991).
 RN [5]
 RP CHARACTERIZATION.
 RA MEDLINE=91317849; PubMed=1860873;
 RA Sakai L.Y., Keene D.R., Glanville R.W., Bachinger H.P.;
 RT "Purification and partial characterization of fibrillin, a cysteine-
 RT rich structural component of connective tissue microfibrils.";
 RL J. Biol. Chem. 266:14763-14770(1991).
 RN [6]
 RP STRUCTURE BY NMR OF 2054-2125.
 RA MEDLINE=98031893; PubMed=9362480;
 RA Yuan X., Downing A.K., Knott V., Handford P.A.;
 RT "Solution structure of the transforming growth factor beta-binding
 RT protein-like module, a domain associated with matrix fibrils.";
 RL EMBO J. 16:6659-6666(1997).
 RN [7]
 RP STRUCTURE BY NMR OF 2124-2205.
 RA MEDLINE=96144829; PubMed=8568869;
 RA Knott V., Downing A.K., Cardy C.M., Handford P.A.;
 RT "Calcium binding properties of an epidermal growth factor-like domain
 RT pair from human fibrillin-1.";
 RL J. Mol. Biol. 255:22-27(1996).
 RN [8]
 RP STRUCTURE BY NMR OF 2124-2205.
 RA MEDLINE=96222301; PubMed=8653794;
 RA Downing A.K., Knott V., Werner J.M., Cardy C.M., Campbell I.D.,
 RA Handford P.A.;
 RT "Solution structure of a pair of calcium-binding epidermal growth
 RT factor-like domains: implications for the Marfan syndrome and other
 RT genetic disorders.";
 RL Cell 85:597-605(1996).
 RN [9]
 RP REVIEW ON MFS VARIANTS.
 RA MEDLINE=96174615; PubMed=8594563;
 RA Collod G., Beroud C., Soussi T., Junien C., Boileau C.;
 RT "Software and database for the analysis of mutations in the human
 RT FBN1 gene.";
 RL Nucleic Acids Res. 24:137-141(1996).
 RN [10]
 RP REVIEW ON MFS VARIANTS.
 RA MEDLINE=97169383; PubMed=9016526;
 RA Collod-Beroud G., Beroud C., Ades L., Black C., Boxer M., Brock D.J.,
 RA Godfrey M., Hayward C., Karttunen L., Milewicz D., Peltonen L.,
 RA Richards R.I., Wang W., Junien C., Boileau C.;
 RT "Marfan database (second edition): software and database for the
 RT analysis of mutations in the human FBN1 gene.";
 RL Nucleic Acids Res. 25:147-150(1997).
 RN [11]
 RP REVIEW ON VARIANTS.
 RA MEDLINE=98062175; PubMed=9401003;
 RA Hayward C., Brock D.J.H.;
 RT "Fibrillin-1 mutations in Marfan syndrome and other type-1
 RT fibrillinopathies.";
 RL Hum. Mutat. 10:415-423(1997).
 RN [12]
 RP VARIANT MFS PRO-1137.
 RA MEDLINE=91304569; PubMed=1852208;
 RA Dietz H.C., Cutting G.R., Pyeritz R.E., Maslen C.L., Sakai L.Y.,
 RA Corson G.M., Puffenberger E.G., Hamosh A., Nanthakumar E.J.,

RA Curristin S.M., Stetren G., Meyers D.A., Francomano C.A.;
 RT "Marfan syndrome caused by a recurrent de novo missense mutation in
 RL the fibrillin gene.";
 RN Nature 352:337-339(1991).
 RP VARIANTS MFS SER-1249; ARG-1663; SBR-2221 AND SER-2307.
 RX MEDLINE=93250894; PubMed=1301946;
 RA Dietz H.C., Saraiya J.M., Pyeritz R.E., Cutting G.R., Francomano C.A.;
 RT "Clustering of fibrillin (FBN1) missense mutations in Marfan syndrome
 RL patients at cysteine residues in EGF-like domains.";
 RN Hum. Mutat. 1:366-374(1992).
 RP VARIANTS MFS SER-2307.
 RX MEDLINE=92235290; PubMed=1569206;
 RA Dietz H.C., Pyeritz R.E., Puffenberger E.G., Kendzior R.U. Jr.,
 RA Corson G.M., Masten C.L., Sakai L.Y., Francomano C.A., Cutting G.R.;
 RT "Marfan phenotype variability in a family segregating a missense
 RL mutation in the epidermal growth factor-like motif of the fibrillin
 gene.";
 RN J. Clin. Invest. 89:1674-1680(1992).
 RP VARIANTS MFS IIE-548 AND ALA-723.
 RX MEDLINE=94010946; PubMed=8406497;
 RA Dietz H.C., McIntosh I., Sakai L.Y., Corson G.M., Chalberg S.C.,
 RA Pyeritz R.E., Francomano C.A.;
 RT "Four novel FBN1 mutations: significance for mutant transcript level
 RL and EGF-like domain calcium binding in the pathogenesis of Marfan
 syndrome.";
 RN Genomics 17:468-475(1993).
 RP VARIANTS MFS SER-2144.
 RX MEDLINE=93278402; PubMed=8504310;
 RA Hewlett D.R., Lynch J.R., Smith R., Sykes B.C.;
 RT "A novel fibrillin mutation in the Marfan syndrome which could
 RL disrupt calcium binding of the epidermal growth factor-like module.";
 RN Hum. Mol. Genet. 2:475-477(1993).
 RP VARIANTS MFS ARG-862; TYR-1117; PRO-1137 AND PHE-1589, AND VARIANT
 RN ALA-1148.
 RX MEDLINE=94108431; PubMed=8281141;
 RA Tyan K., Comeau K., Pearson M., Wilgenbus P., Levitt D., Gassner C.,
 RA Berg M.A., Miller D.C., Francke U.;
 RT "Mutation screening of complete fibrillin-1 coding sequence: report
 RL of five new mutations, including two in 8-cysteine domains.";
 RN Hum. Mol. Genet. 2:1813-1821(1993).
 RP VARIANTS MFS GLY-217 AND ARG-2627.
 RX MEDLINE=95067970; PubMed=7977366;
 RA Karttunen L., Ragnunath M., Loennqvist L., Peltonen L.;
 RT "A compound-heterozygous Marfan patient: two defective fibrillin
 RL alleles result in a lethal phenotype.";
 RN Am. J. Hum. Genet. 55:1083-1091(1994).
 RP VARIANTS EL LYS-2447.
 RX MEDLINE=94245249; PubMed=8188302;
 RA Loennqvist L., Child A., Kainulainen K., Davidson R., Puhakka L.,
 RA Peltonen L.;
 RT "A novel mutation of the fibrillin gene causing ectopia lentis.";
 RN Genomics 19:573-576(1994).
 RP VARIANTS MFS CVS-627.
 RX MEDLINE=94272487; PubMed=8004112;
 RA Hayward C., Rae A.L., Porteous M.E.M., Logie L.J., Brock L.J.;
 RT "Two novel mutations and a neutral polymorphism in EGF-like domains
 RL of the fibrillin gene (FBN1): SSCP screening of exons 15-21 in Marfan
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 RN Hum. Mol. Genet. 3:373-375(1994).
 RP VARIANTS MFS CVS-122.
 RX MEDLINE=94314977; PubMed=8040326;
 RA Stahl-Hallengren C., Ukkonen T., Kainulainen K., Kristofersson U.,
 RA Saxne T., Tornqvist K., Peltonen L.;
 RT "An extra cysteine in one of the non-calcium-binding epidermal growth
 RL

RT factor-like motifs of the FBN1 polypeptide is connected to a novel
 RT variant of Marfan syndrome.";
 RL J. Clin. Invest. 94:709-713(1994).
 RN [121]
 RP VARIANTS MFS TYR-1223.
 RX MEDLINE=94351682; PubMed=8071963;
 RA Hewlett D.R., Lynch J.R., Child A., Sykes B.C.;
 RT "A new missense mutation of fibrillin in a patient with Marfan
 RL syndrome.";
 RN J. Med. Genet. 31:338-339(1994).
 RP VARIANTS MFS HTS-1170.
 RX MEDLINE=95174777; PubMed=7870075;
 RA Hayward C., Porteous M.E.M., Brock D.J.H.;
 RT "A novel mutation in the fibrillin gene (FBN1) in familial
 RL arachmodactyly.";
 RN Mol. Cell. Probes 8:325-327(1994).
 RP VARIANTS MFS GLY-217; ASN-1023; ARG-1074; TYR-1242; ARG-1513;
 RP GLU-2127; TRP-2151; LYS-2447 AND ARG-2511.
 RX MEDLINE=94184368; PubMed=8136837;
 RA Kainulainen K., Karttunen L., Puhakka L., Sakai L., Peltonen L.;
 RT "Mutations in the fibrillin gene responsible for dominant ectopia
 RL lentis and neonatal Marfan syndrome.";
 RN Nat. Genet. 6:64-69(1994).
 RN [125]
 Query Match 11.7%; Score 176.5; DB 1; Length 2871;
 Best Local Similarity 22.7%; Pred. No. 9.1e-06;
 Matches 59; Conservative 19; Mismatches 79; Indels 103; Gaps 8;
 QY 26 PGRRYCAVARAGDPPVSESVQRYVQPFLLTDCGHR---ACSTYRTIYRTAVRSPGLAPA 82
 DB 75 PGNOCIVPIPIGRHSQGDGFCR---PNNCTPSPQIAPSCGS-RSICMCRNMNGSGCS 130
 QY 83 RPRVACPCWKRRTSGLPGACAAITCQPPCRNNGSCVQFGRGRCPAWFGDTQC----- 135
 DB 131 DDHCLCQKQGYIGTH-----CGQPVCESSGLNNGRCVABNRCACTYGFPGQCCERDYRTGP 185
 QY 136 -----S 136
 DB 186 CFTVISNMQCGQSLGIVCTKQLCCATVGRAMGHPCEMCPAQPPHRCRRRTPINIRTAGCQ 245
 QY 137 DVDECSARRGSCP-ORCINTAGSYWQCQEGHSLSADDTLC-----VPRKG--- 181
 DB 246 DVDECGALPGICQGGNCINTVYGSFECRCPAHKINKNEVSKCEDIDECSTIRGICGGGECT 305
 QY 182 -----PPRVAANPTG 191
 DB 306 NTVSSYFPCPCPPGFYTSBDG 325
 RESULT 11
 NTC3_HUMAN
 ID NTC3_HUMAN STANDARD; PRT; 2321 AA.
 AC Q9UM47; OSUBEB3; OSUPL3; O9Y6L8;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 GN Neurogenic locus notch homolog protein 3 precursor (Notch 3).
 DN NOTCH3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NCBI_TaxID:9606;
 RN [11]
 RP SEQUENCE FROM N.A. PubMed=8878478;
 RX MEDLINE=97032728;
 RA Joutel A., Corpechot C., Ducros A., Vahedi K., Chabriat H., Mouton P.,
 RA Alanowitch S., Demenga V., Cecillion M., Marechal E., Maciazek J.,
 RA Vaysiere C., Crnaud C., Cabanis E.-A., Ruchoux M.M., Weissenbach J.,
 RA Bach J.-F., Boussemer M.-G., Tournier-Lasserre E.;
 RT "Notch3 mutations in CADASIL, a hereditary adult-onset condition

RT causing stroke and dementia.":
 RL Nature 383:707-710(1996).
 RP SEQUENCE FROM N.A.
 RA Gurel M., Artavanis-Tsakonas S.;
 RL Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.
 RP [3]
 RA SEQUENCE FROM N.A.
 RA Lamerdin J.E., McCreedy P.M., Skowronski E., Adamson A.W.,
 RA Burkhart-Schultz K., Gordon L., Kyle A., Ramirez M., Stilaagen S.,
 RA Phan H., Velasco N., Gaines J., Dargahan L., Poundstone P.,
 RA Christensen M., Georgescu A., Avila J., Liu S., Atlix C., Andreise T.,
 RA Trankheim M., Amico-Keller G., Coefield J., Duarte S., Lucas S.,
 RA Bruce R., Thomas P., Quan G., Krommiller B., Arellano A.,
 RA Montgomery M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.S.,
 RA Carrano A.V.;
 RA "Sequence analysis of an 1.5 Mb olfactory receptor (OLFR) cluster in
 RT 19p13.1";
 RL Submitted (May-1998) to the EMBL/GenBank/DBJ databases.
 RP [4]
 RA VARIANTS CADASIL TYR-49; CYS-71; CYS-90; CYS-110; CYS-133; CYS-141;
 RP ARG-146; CYS-153; CYS-169; CYS-171; CYS-182; ARG-185; SER-212;
 RP GLY-222; TYR-224; CYS-258; TYR-542; CYS-558; CYS-578; CYS-728;
 RP CYS-985; CYS-1006; CYS-1031; CYS-1231 AND ARG-1261, AND VARIANTS
 RP ARG-170; LEU-496; GLN-1133; MET-1183 AND ALA-2223.
 RA MEDLINE=98049753; PubMed=9388399;
 RA Joutel A., Vahedi K., Corpechot C., Troesch A., Chabriat H.,
 RA Vaysiere C., Cruaud C., Maciazek J., Weissenbach J., Bousser M.-G.,
 RA Bach J.-F., Tourner-Lasserre E.;
 RT "Strong clustering and stereotyped nature of Notch3 mutations in
 RT CADASIL patients.";
 RL Lancet 350:1511-1515(1997).
 RP [5]
 RA VARIANT CADASIL 114-GLY-PRO-120 DEL.
 RP MEDLINE=20264473; PubMed=10802807.
 RA Joutel A., Chabriat H., Vahedi K., Domenga V., Vaysiere C.,
 RA Ruchoux M.M., Lucas C., Lays D., Bousser M.-G., Tourner-Lasserre E.;
 RT "Splice site mutation causing a seven amino acid Notch3 in-frame
 RT deletion in CADASIL.";
 RL Neurology 54:1874-1875(2000).
 RP [6]
 RA IDENTIFICATION OF LIGANDS.
 RX MEDLINE=99180765; PubMed=10079256;
 RA Gray G.E., Mann R.S., Mitsiadis E., Henrique D., Carcangiu M.-L.,
 RA Banks A., Lehman J., Ward D., Ish-Horowitz D., Artavanis-Tsakonas S.;
 RT "Human ligands of the Notch receptor.";
 RL Am. J. Pathol. 154:785-794(1999).
 CC -1- FUNCTION: Functions as a receptor for membrane-bound ligands
 CC Jagged1, Jagged2 and Delta to regulate cell-fate determination.
 CC Upon ligand activation through the released notch intracellular
 CC domain (NICD) it forms a transcriptional activator complex with
 CC RBP-J kappa and activates genes of the enhancer of split locus.
 CC Affects the implementation of differentiation, proliferation and
 CC apoptotic programs (By similarity).
 CC -1- SUBUNIT: Heterodimer of a C-terminal fragment N(TM) and a N-
 CC terminal fragment N(EC) which are probably linked by disulfide
 CC bonds (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein. Following
 CC proteolytical processing NICD is translocated to the nucleus.
 CC -1- TISSUE SPECIFICITY: Ubiquitously expressed in fetal and adult
 CC tissues.
 CC -1- PTM: Synthesized in the endoplasmic reticulum as an inactive form
 CC which is proteolytically cleaved by a furin-like convertase in the
 CC trans-Golgi network before it reaches the plasma membrane to yield
 CC an active, ligand-accessible form. Cleavage results in a C-
 CC terminal fragment N(TM) and a N-terminal fragment N(EC). Following
 CC ligand binding, it is cleaved by TNF-alpha converting enzyme
 CC (TACE) to yield a membrane-associated intermediate fragment called
 CC notch extracellular truncation (NEXT). This fragment is then
 CC cleaved by presenilin dependent gamma-secretase to release a
 CC notch-derived peptide containing the intracellular domain (NICD)
 CC from the membrane (By similarity).
 CC -1- PTM: Phosphorylated (By similarity).

CC -1- DISEASE: Defects in NOTCH3 are associated with CADASIL (Cerebral
 CC autosomal dominant arteriopathy with subcortical infarcts and
 CC leukoencephalopathy) which causes a type of stroke and dementia of
 CC which key features include recurrent subcortical ischemic events
 CC and vascular dementia.
 CC -1- SIMILARITY: BELONGS TO THE NOTCH FAMILY.
 CC -1- SIMILARITY: Contains 34 EGF-like domains.
 CC -1- SIMILARITY: Contains 3 Lin/Notch repeats.
 CC -1- SIMILARITY: Contains 5 ANK repeats.
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 CC -----
 DR EMBL; U97669; AAB91371.1; .
 DR EMBL; AF058900; AAC14346.1; .
 DR EMBL; AF058881; AAC14346.1; JOINED.
 DR EMBL; AF058882; AAC14346.1; JOINED.
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 DR EMBL; AF058885; AAC14346.1; JOINED.
 DR EMBL; AF058886; AAC14346.1; JOINED.
 DR EMBL; AF058887; AAC14346.1; JOINED.
 DR EMBL; AF058888; AAC14346.1; JOINED.
 DR EMBL; AF058889; AAC14346.1; JOINED.
 DR EMBL; AF058890; AAC14346.1; JOINED.
 DR EMBL; AF058891; AAC14346.1; JOINED.
 DR EMBL; AF058892; AAC14346.1; JOINED.
 DR EMBL; AF058893; AAC14346.1; JOINED.
 DR EMBL; AF058894; AAC14346.1; JOINED.
 DR EMBL; AF058895; AAC14346.1; JOINED.
 DR EMBL; AF058896; AAC14346.1; JOINED.
 DR EMBL; AF058897; AAC14346.1; JOINED.
 DR EMBL; AF058898; AAC14346.1; JOINED.
 DR EMBL; AF058899; AAC14346.1; JOINED.
 DR EMBL; AC004257; AAC04897.1; .
 DR EMBL; AC004663; AAC15789.1; ALT_INIT.
 DR PIR; S78549; S78549.
 DR HSSP; P00740; 1EDM.
 DR GENEW; HGNC:7883; NOTCH3.
 DR MIM; 600276; .
 DR MIM; 125310; .
 DR InterPro; IPR002110; ANK.
 DR InterPro; IPR000152; Asx_hydroxy1.
 DR InterPro; IPR000742; EGF_2.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR001438; EGF_11.
 DR InterPro; IPR006209; EGF_like.
 DR InterPro; IPR002049; LamInn_EGF.
 DR InterPro; IPR000800; Notch.
 DR Pfam; PF00023; ank; 6.
 DR Pfam; PF00008; EGF; 34.
 DR Pfam; PF00066; notch; 3.
 DR PRINTS; PR00010; EGFBLD.
 DR PRINTS; PR00011; EGF_LAMININ.
 DR PRINTS; PR01452; NOTCH.
 DR SMART; SM00248; ANK; 6.
 DR SMART; SM00179; EGF_CA; 19.
 DR SMART; SM00004; NL; 3.
 DR PROSITE; PS50088; ANK_REPEAT; 4.
 DR PROSITE; PS50297; ANK_REP_REGION; 1.
 DR PROSITE; PS00010; ASX_HYDROXYL; 18.
 DR PROSITE; PS00022; EGF_1; 33.
 DR PROSITE; PS01186; EGF_2; 25.
 DR PROSITE; PS01187; EGF_CA; 16.
 KW Receptor; Transcription regulation; Activator; Differentiation;
 KW Developmental protein; Repeat; ANK repeat; EGF-like domain;
 KW Transmembrane; Glycoprotein; Signal; Phosphorylation; Polymorphism;
 KW Disease mutation.

FT	SIGNAL	1	39	POTENTIAL.
FT	CHAIN	40	2321	NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 3.
FT	CHAIN	1629	2321	NOTCH EXTRACELLULAR TRUNCATION (BY SIMILARITY).
FT	CHAIN	1662	2321	NOTCH INTRACELLULAR DOMAIN (BY SIMILARITY).
FT	DOMAIN	40	1643	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	1644	1664	POTENTIAL.
FT	DOMAIN	1665	2321	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	40	777	EGF-LIKE 1.
FT	DOMAIN	78	118	EGF-LIKE 2.
FT	DOMAIN	119	156	EGF-LIKE 3.
FT	DOMAIN	158	195	EGF-LIKE 4.
FT	DOMAIN	197	234	CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	236	272	EGF-LIKE 5.
FT	DOMAIN	274	312	EGF-LIKE 6.
FT	DOMAIN	314	350	EGF-LIKE 7.
FT	DOMAIN	351	389	EGF-LIKE 8.
FT	DOMAIN	391	429	EGF-LIKE 9.
FT	DOMAIN	431	467	CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	469	505	EGF-LIKE 10.
FT	DOMAIN	507	543	CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	545	580	EGF-LIKE 11.
FT	DOMAIN	582	618	CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	620	655	EGF-LIKE 12.
FT	DOMAIN	657	693	CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	695	730	EGF-LIKE 13.
FT	DOMAIN	734	770	EGF-LIKE 14.
FT	DOMAIN	771	808	EGF-LIKE 15.
FT	DOMAIN	810	847	CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	849	885	EGF-LIKE 16.
FT	DOMAIN	887	922	CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	924	960	EGF-LIKE 17.
FT	DOMAIN	962	998	EGF-LIKE 18.
FT	DOMAIN	1000	1034	EGF-LIKE 19.

Query Match 11.7%; Score 175.5; DB 1; Length 2321;
 Best Local Similarity 34.5%; Pred. No. 8.8e-06;
 Matches 50; Conservative 14; Mismatches 44; Indels 37; Gaps 11;

QY	56	CDGHRACSTYRTYRTRARRSPGLAPRRVYAC-CGQWKR--TSGLPAGCAATCOPPCR	112	SVVAGTARFSCRCRGRGFGPDCSIPDDPC---LSSPCA	129
DB	87	CAARGVQCS-----			
QY	113	NGSSC-VOP-GR--CRCPPAGRGDTCCOSVDDEC-----SARGGCCPQRCINTAGSYWCQCM	164		
DB	130	HGARCIVGPDGRFLCCGPFYQGRSCRSDVDEBRCVGEPPCRHG--TCLNTPRSFRCCQCP	186		
QY	165	EGHSLADGTLVCKGKGGPPRVADNP	189		
DB	187	AGYT-----GFLCENPAVP--CAKSP	205		

RT C1q/MBL/SPA receptor that mediates enhanced phagocytosis in vitro. ;
 RL Immunity 6:119-129(1997).
 RN [2]
 RP SEQUENCE FROM N.A., AND VARIANT ALA-318.
 RX MEDLINE=21640567; PubMed=11781389;
 RA Steinberger P., Szekeres A., Wille S., Stockl J., Selenko N.,
 Prager E., Staffler G., Madic O., Stockinger H., Knapp W.;
 RT "Identification of human CD93 as the phagocytic C1q receptor (C1qRp)
 by expression cloning." ;
 RL J. Leukoc. Biol. 71:133-140(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21638749; PubMed=11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 Jones M., Stavriliadis G., Almeida J.P., Babbage A.K., Bagguley C.L.,
 Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
 Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
 Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 Clegg S., Cobley V.E., Collier R.E., Connor R.E., Copby N.R.,
 Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
 Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 Grainger D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 Leharshashko M.H., Leverisha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 Marsh V.L., Martin S.L., McCormack L.J., McIay K., McMurtry A.A.,
 Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 Oliver K., Parker A., Patel T., Pearce T.A.V., Peck A.I.,
 Phillimore B.J.C.T., Prichallingam S.R., Plumb R.W., Ramsay H.,
 Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkheen R., Sims S.,
 Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Stulson J.E.,
 Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 Tracey A., Tomams A.C., Vaudin M., Wall M., Wallis J.M.,
 Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 Wilmshurst L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.A.,
 Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20." ;
 RL Nature 414:865-871(2001).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klansner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Scheeter C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Usslin T.B., Toshiyuki S., Carninci P., Pritchard S.,
 Raha S.S., Loguelano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 Bosak S.A., McEwan P.J., McKernan K.J., Malek A.M., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultky S.W.,
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X.M., Gibbs R.A.,
 Fahy J., Hellon E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,
 Butlerfield Y.S.N., Krzywinski M.I., Skalska J., Smalins D.E.,
 Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 human and mouse cDNA sequences." ;
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP CHARACTERIZATION.
 RX MEDLINE=21990337; PubMed=11994479;
 RA McGreal E.P., Ikekaki N., Akatsu H., Morgan B.P., Gasque P.;
 RT "Human C1qRp is identical with CD93 and the mnt-11 antigen but does
 not bind C1q." ;
 RL J. Immunol. 168:5222-5232(2002).
 RN [6]
 RP O-GLYCOSYLATION.

RA MEDLINE=99192777; PubMed=10092817;
 RA Nepomuceno R.R., Ruiz S., Park M., Renner A.J.;
 RT "Clqmc is a heavily O-glycosylated cell surface protein involved in
 RT the regulation of phagocytic activity.";
 RL J. Immunol. 162:3583-3589(1999).
 CC -1- FUNCTION: Receptor (or element of a larger receptor complex) for
 CC Clq, mannose-binding lectin (MBL) and pulmonary surfactant
 CC protein A (SPA). May mediate the enhancement of phagocytosis in
 CC collagen. May play a role in intercellular adhesion.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: Highly expressed in endothelial cells,
 CC platelets, cells of myeloid origin, such as monocytes and
 CC neutrophils. Not expressed in cells of lymphoid origin.
 CC -1- PFM: N- and O-glycosylated.
 CC -1- SIMILARITY: Contains I C-type lectin family domain.
 CC -1- SIMILARITY: Contains 5 EGF-like domains.
 CC -1- CAUTION: Has been sometimes referred to as a collectin receptor.
 CC -1- CAUTION: According to Ref.5, Clq is not a ligand for ClqR1.
 CC -1- DATABASE: NAME=PROW; NOTE=PROW 3:1-6(2001);
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/guide/467246456_g.htm".
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U94333; AAB53110.1; -;
 DR EMBL; AL118508; CAC00597.1; -;
 DR EMBL; BC028075; AAH28075.1; -;
 DR HSSP; P35555; IEMN.
 DR GeneW; HGNC:15855; ClqR1.
 DR MIM; 120577; -;
 DR GO; GO:0016021; C:integral to membrane; IC.
 DR GO; GO:0004872; F:receptor activity; NAS.
 DR GO; GO:0016337; P:cell-cell adhesion; IDA.
 DR GO; GO:0042116; P:macrophage activation; NAS.
 DR GO; GO:006909; P:phagocytosis; NAS.
 DR InterPro; IPR00152; Asx hydroxyl.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR006209; EGF_Like.
 DR InterPro; IPR001304; Lectin_C.
 DR Pfam; PF00008; EGF; 5.
 DR Pfam; PF00059; Lectin_C; 1.
 DR Pfam; PF01108; Tissue_fac; 1.
 DR SMART; SM00034; CLECT; 1.
 DR SMART; SM00179; EGF_CA; 3.
 DR PROSITE; PS00010; ASX_HYDROXYL; 3.
 DR PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
 DR PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
 DR PROSITE; PS50186; EGF_2; 3.
 DR PROSITE; PS01187; EGF_CA; 3.
 KW Cell adhesion; Receptor; Repeat; Signal; Transmembrane;
 KW EGF-like domain; Lectin; Glycoprotein; Polymorphism.
 KM EGF_LIKE 1 21
 FT CHAIN 1 21
 FT DOMAIN 24 580
 FT TRANSMM 581 601
 FT DOMAIN 602 652
 FT DOMAIN 32 174
 FT DOMAIN 260 301
 FT DOMAIN 302 344
 FT DOMAIN 345 384
 FT DOMAIN 385 426
 FT DOMAIN 427 468
 FT DOMAIN 594 601
 FT DISULFID 264 275
 FT DISULFID 271 285
 FT DISULFID 287 300
 FT DISULFID 306 317

FT DISULFID 311 328 BY SIMILARITY.
 FT DISULFID 330 343 BY SIMILARITY.
 FT DISULFID 349 358 BY SIMILARITY.
 FT DISULFID 354 367 BY SIMILARITY.
 FT DISULFID 369 383 BY SIMILARITY.
 FT DISULFID 389 400 BY SIMILARITY.
 FT DISULFID 396 409 BY SIMILARITY.
 FT DISULFID 411 425 BY SIMILARITY.
 FT DISULFID 431 443 BY SIMILARITY.
 FT DISULFID 439 452 BY SIMILARITY.
 FT DISULFID 454 467 BY SIMILARITY.
 FT CAROHYD 325 325 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 318 318 V->A.
 FT CONFLICT 22 22 /FTID=VAR_013573.
 FT CONFLICT 36 36 T->V (IN REF. 1; AA SEQUENCE).
 FT CONFLICT 38 39 C->T (IN REF. 1; AA SEQUENCE).
 FT CONFLICT 155 155 TA->R (IN REF. 1; AA SEQUENCE).
 FT CONFLICT 186 186 S->N (IN REF. 1).
 FT CONFLICT 492 492 G->A (IN REF. 1; AA SEQUENCE).
 FT CONFLICT 496 496 S->A (IN REF. 1; AA SEQUENCE).
 FT CONFLICT 504 504 R->O (IN REF. 1; AA SEQUENCE).
 FT CONFLICT 541 541 P->G (IN REF. 1; AA SEQUENCE).
 SQ SEQUENCE 652 AA; 68560 MW; EBCA0FEAC55FCAC2 CRC64;
 Query Match 11.6%; Score 175; DB 1; Length 652;
 Best Local Similarity 33.1%; Pred. No. 2.6e-06;
 Matches 60; Conservative 10; Mismatches 57; Indels 54; Gaps 13;
 QY 25 RPPRRV-----CAVRAHGDVPSBSFYQVRYQVPLFTTCDGHRACSTYRTYRTRAVRSPG 78
 DB 288 RPPFRLLDVLVTCASR---NPPCSSS-----PGRGATCV----- 318
 QY 79 LAPARPRAC-CP-GMRTSGLPACGAATQ-PPCRNGSCVQ-PG--RRCRPAQR-- 130
 DB 319 LGPHGKNVTCRCPOGYQDSSQLDCVDVDEQDSDPCAC--BCVTPPGFRCECWGYPBG 376
 QY 131 --GDTQGSVDVECSARRGCGCPORCINTAGSYWCQCEGHSLSA-DGTL-----CVPKGG 181
 DB 377 GPGEACQDVDECALGRSPCAQCGTNTGDSFHCSEBTVYLAAGEITGQCDVDECVGFGG 436
 QY 182 P 182
 DB 437 P 437
 RESULT 13
 NOTC DROME STANDARD; PRT; 2703 AA.
 AC P07207; 097458; P04154; Q9W4T9;
 DT 01-NOV-1986 (Rel. 03, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Neurogenic locus Notch protein precursor.
 GN N OR EG:140G11.1 OR EG:163M10.2 OR CG39396.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N. A.
 RC STRAIN=Oregon-R; TISSUE=Embryo;
 RC MEDLINE=86079539; PubMed=3935325;
 RA Wharton K.A., Johansen K.M., Xu T., Artavanis-Tsakonas S.;
 RT "Nucleotide sequence from the neurogenic locus notch implies a gene
 RT product that shares homology with proteins containing EGF-like
 RT repeats.";
 RL Cell 43:567-581(1985).
 RN [2]
 RP SEQUENCE FROM N. A.
 RC STRAIN=Canton-S; and Oregon-R; TISSUE=Embryo;
 RC MEDLINE=87064624; PubMed=3097517;
 RX

RA Kidd S., Kelley M.R., Young M.W. ;
RT "Sequence of the notch locus of Drosophila melanogaster: relationship
RL of the encoded protein to mammalian clotting and growth factors." ;
RM Mol. Cell. Biol. 6:3094-3108(1986).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Cocayne J.D.,
RA Amaralides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Suton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blaise R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Prankoch C., Baldwin D.,
RA Ballew R.W., Basu A., Baxendale J., Bayraktaroglu U., Beaulieu E.M.,
RA Beeson K.Y., Benos P.V., Beyman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Dupont L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durkin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hosrin D., Houston K.A., Howland T.J., Mei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Kapen G.H., Ke Z., Kemison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasro P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Moharry C., Morris J., Mostreli A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Teclor C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C. ;
RT "The genome sequence of Drosophila melanogaster." ;
RL Science 287:2185-2195(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Oregon-R;
RX MEDLINE=20196011; PubMed=10731137;
RA Benos P.V., Galt M.K., Ashburner M., Murphy L., Harris D.,
RA Barrell B.G., Ferraz C., Vidal S., Brunn C., Demallies J., Cadieu E.,
RA Dreano S., Gloux S., Lelaure V., Nottler S., Galibert F., Bokkova L.,
RA Minana B., Kataros F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
RA Papagiannakis G., Spanos L., Cox S., Maduno E., de Pablo B.,
RA Modolell J., Peter A., Schoettler P., Werner M., Mourikioti F.,
RA Beilner N., Dowe G., Schaefer U., Jaeckle H., Bucheton A.,
RA Callister D.M., Campbell L.A., Darlamitsova A., Henderson N.S.,
RA McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
RA Glover D.M. ;
RT "From sequence to chromosome: the tip of the X chromosome of D.
RL melanogaster." ;
RM Science 287:2220-2222(2000).
RN [5]
RP SEQUENCE OF 2505-2611 FROM N.A.
RC MEDLINE=85099329; PubMed=2981631;
RX Wharton K.A., Yedvobnick B., Finnerty V.G., Artavanis-Tsakonas S. ;
RT "opa: a novel family of transcribed repeats shared by the Notch locus
RL and other developmentally regulated loci in D. melanogaster." ;
RM Cell 40:55-62(1985).
RN [6]
RP *SEQUENCE OF 1-8 FROM N.A.
RC MEDLINE=87257846; PubMed=3037327;

RA Kelley M.R., Kidd S., Berg R.L., Young M.W. ;
RT "Restriction of P-element insertions at the Notch locus of Drosophila
RL melanogaster." ;
RM Mol. Cell. Biol. 7:1545-1548(1987).
RN [7]
RP REVIEW.
RA "Many cell types specified by Notch function." ;
RL Curr. Biol. 1:120-122(1991).
RT -1- FUNCTION: Functions as a receptor for membrane-bound ligands Delta
CC and Serrate to regulate cell-fate determination. Upon ligand
CC activation through the released notch intracellular domain (NICD)
CC it forms a transcriptional activator complex with Su(H)
CC (Suppressor of hairless) and activates genes of the enhancer of
CC split locus. Essential for proper differentiation of ectoderm.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: BELONGS TO THE NOTCH FAMILY.
CC -1- SIMILARITY: Contains 36 EGF-like domains.
CC -1- SIMILARITY: Contains 3 Lin/Notch repeats.
CC -1- SIMILARITY: Contains 6 ANK repeats.
CC -----
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CC -----
DR EMBL: M16152; AAB59220.1; -
DR EMBL: M16153; AAB59220.1; JOINED.
DR EMBL: M16149; AAB59220.1; JOINED.
DR EMBL: M16150; AAB59220.1; JOINED.
DR EMBL: M16151; AAB59220.1; JOINED.
DR EMBL: K03508; AAA28725.1; -
DR EMBL: M13689; AAA28725.1; JOINED.
DR EMBL: K03507; AAA28725.1; JOINED.
DR EMBL: AE003426; AAF45848.2; -
DR EMBL: AL035395; CAB37610.1; JOINED.
DR EMBL: M12175; AAA74496.1; -
DR EMBL: M16025; AAA28726.1; -
DR PIR: A24420; A24420.
DR HSSP: P00740; 1EDM.
DR FLYBase: FBgn0004647; N.
DR GO: GO:0005634; C:nucleus; NAS.
DR GO: GO:0005886; C:plasma membrane; IDA.
DR GO: GO:0004888; F:transmembrane receptor activity; NAS.
DR GO: GO:0007403; P:determination of glial fate; IMP.
DR GO: GO:0007293; P:egg chamber formation; IMP.
DR GO: GO:0042067; P:establishment of commatidial polarity (sensu. . .); NAS.
DR GO: GO:0046331; P:lateral inhibition; NAS.
DR GO: GO:0007498; P:mesoderm development; IMP.
DR GO: GO:0007519; P:myogenesis; IMP.
DR GO: GO:0046329; P:negative regulation of JNK cascade; NAS.
DR GO: GO:0045465; P:R8 differentiation; NAS.
DR GO: GO:0045468; P:regulation of R8 spacing; NAS.
DR GO: GO:0007423; P:sensory organ development; IMP.
DR GO: GO:0007424; P:tracheal system development (sensu Insecta); NAS.
DR GO: GO:0007476; P:wing morphogenesis; NAS.
DR InterPro: IPR00152; Asx_Hydroxyl.
DR InterPro: IPR000742; EGF_2.
DR InterPro: IPR001881; EGF_Ca.
DR InterPro: IPR001438; EGF_T1.
DR InterPro: IPR006209; EGF_Like.
DR InterPro: IPR020449; Laminin_EGF.
DR InterPro: IPR000800; Notch.
DR Pfam: PF00023; ank; 7.
DR Pfam: PF00008; EGF; 36.
DR Pfam: PF00066; notch; 3.
DR PRINTS: PR00010; EGFBL00D.
DR PRINTS: PR00011; EGFBLAMININ.

PRINTS; PRO1452; NOTCH.
 SMART; SM00248; ANK; 7.
 SMART; SM00179; EGF_CA; 24.
 SMART; SM00004; NID; 3.
 PROSITE; PS50068; ANK_REPEAT; 5.
 PROSITE; PS50297; ANK_REPEAT_REGION; 1.
 PROSITE; PS00010; ASX_HYDROXYL; 22.
 PROSITE; PS00022; EGF_1; 34.
 PROSITE; PS01186; EGF_2; 28.
 PROSITE; PS01187; EGF_CA; 21.
 Receptor; Transcription regulation; Activator; Differentiation;
 Developmental protein; Neurogenesis; Repeat; ANK repeat;
 EGF-like domain; Transmembrane; Glycoprotein; Signal.
 SIGNAL
 CHAIN 1 44
 FT DOMAIN 45 2703 NEUROGENIC LOCUS NOTCH PROTEIN.
 FT TRANSMEM 1746 1745 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 1767 1766 POTENTIAL.
 FT DOMAIN 1767 2703 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 96 95 EGF-LIKE 1.
 FT DOMAIN 136 136 EGF-LIKE 2.
 FT DOMAIN 176 176 EGF-LIKE 3.
 FT DOMAIN 215 215 EGF-LIKE 4.
 FT DOMAIN 217 253 CALCIUM-BINDING (POTENTIAL).
 FT DOMAIN 255 255 EGF-LIKE 5.
 FT DOMAIN 293 291 EGF-LIKE 6.
 FT DOMAIN 331 329 EGF-LIKE 7.
 FT DOMAIN 370 370 EGF-LIKE 8.
 FT DOMAIN 408 408 EGF-LIKE 9.
 FT DOMAIN 409 447 EGF-LIKE 10.
 FT DOMAIN 449 486 EGF-LIKE 11. CALCIUM-BINDING (POTENTIAL).

Query Match 11.6%; Score 175; DB 1; Length 2703;
 Beet Local Similarity 25.3%; Pred. No. 1.1e-05;
 Matches 57; Conservative 22; Mismatches 62; Indels 84; Gaps 13;

OY 18 GSTEHAHYPPRRVCAVRRAH-GDPVSESEFVQVYQFPFLTTCGHRACSTYRT---YKRT 71
 DB 70 GGTCTVQLNGKTYKCDSDSHYVD-----YCHHRNPDCNSMRCONGATQCV 113
 OY 72 AYRRAEPLAAPPARRAC-CP-GWKRT---SGLRGACGAALC----- 107
 DB 114 TFRN-----GRFGISCKCPLEFDSLCEIAVPAACDHYTCTANGSTCQKTLREYTCACA 167
 OY 108 -----QPPCRNGSCV-----QPRGCRCPAGWRGDTCCSDVDECSA---R 144
 DB 168 NGYTERCETKNLCASSPCRNATCTALAGSSSFCSQCPGPTGDTGVDIECCGSPCK 227
 OY 145 RGGCPQRCINRAGSYWCOCWBSHSLSADGTLCPKGGPPRYAANP 189
 DB 228 YGG--TCVNTHGSIYQCWCPCPTGYT-----GKDCDTRKYP--CSPSP 263

RESULT 14
 NIDO_HUMAN STANDARD; PRT; 1247 AA.
 ID NIDO_HUMAN
 AC P14543; Q14942;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Nidogen precursor (Entactin).
 GN NID.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Euhetera; Primates; Carnivora; Hominoidea; Homo.
 CC NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90091745; Pubmed=2574658;
 RA Nagayoshi T., Sanborn D., Hickok N.J., Olsen D.R., Fazio M.J.,
 RA Chh M.-L., Knowlton R., Mann K., Deutzmann R., Timpl R., Uitto J.;
 RT "Human nidogen: complete amino acid sequence and structural domains
 RT deduced from cDNAs, and evidence for polymorphism of the gene."
 RL DNA 8:581-594(1989).
 RN [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE=96044428; Pubmed=7557988;
 RA Zimmermann K., Holschen S., Hafner M., Nischt R.;
 RT "Genomic sequences and structural organization of the human nidogen
 RT gene (NID)."
 RL Genomics 27:245-250(1995).
 RN [3]
 RP SEQUENCE OF 667-1247 FROM N.A.
 RC TISSUE=placenta;
 RX MEDLINE=89770475; Pubmed=2471408;
 RA Olsen D.R., Nagayoshi T., Fazio M., Mattei M.-G., Passage E., Weil D.,
 RA Timpl R., Chu M.L., Uitto J.;
 RT "Human nidogen: cDNA cloning, cellular expression, and mapping of the
 RT gene to chromosome 14q33."
 RL Am. J. Hum. Genet. 44:876-885(1989).
 CC -1- FUNCTION: SUFATED GLYCOPROTEIN WHICH IS WIDELY DISTRIBUTED IN
 CC BASEMENT MEMBRANES AND THAT IS TIGHTLY ASSOCIATED WITH LAMININ.
 CC ALSO BINDS TO COLLAGEN IV. IT PROBABLY HAS A ROLE IN CELL-
 CC EXTRACELLULAR MATRIX INTERACTIONS.
 CC -1- SUBUNIT: Interacts with FNBI (By similarity).
 CC -1- SUBCELLULAR LOCATION: BASEMENT MEMBRANES.
 CC -1- PTM: N- AND O-GLYCOSYLATED.
 CC -1- SIMILARITY: Contains 6 EGF-like domains.
 CC -1- SIMILARITY: Contains 1 thyroglobulin type-1 domain.
 CC -1- SIMILARITY: Contains 5 LDL-receptor YWTD domains.
 CC -----
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CC EMBL; M30269; AA5932.1; .
 CC EMBL; X82245; CA57709.1; JOINED.
 CC EMBL; X84819; CA57709.1; JOINED.
 CC EMBL; X84820; CA57709.1; JOINED.
 CC EMBL; X84821; CA57709.1; JOINED.
 CC EMBL; X84822; CA57709.1; JOINED.
 CC EMBL; X84823; CA57709.1; JOINED.
 CC EMBL; X84824; CA57709.1; JOINED.
 CC EMBL; X84825; CA57709.1; JOINED.
 CC EMBL; X84826; CA57709.1; JOINED.
 CC EMBL; X84827; CA57709.1; JOINED.
 CC EMBL; X84828; CA57709.1; JOINED.
 CC EMBL; X84829; CA57709.1; JOINED.
 CC EMBL; X84830; CA57709.1; JOINED.
 CC EMBL; X84831; CA57709.1; JOINED.
 CC EMBL; X84832; CA57709.1; JOINED.
 CC EMBL; X84833; CA57709.1; JOINED.
 CC EMBL; X84834; CA57709.1; JOINED.
 CC EMBL; X84835; CA57709.1; JOINED.
 CC EMBL; X84836; CA57709.1; JOINED.
 CC EMBL; X84837; CA57709.1; JOINED.
 CC EMBL; M27445; AA57261.1; .
 CC PIR; A33322; MIMHND.
 CC PDB; 1NDX; 29-DEC-99.
 CC GeneW; HGNC:7821; NID.
 CC MIM; 131390; .
 CC InterPro; IPR000152; Asx hydroxyl.
 CC InterPro; IPR001881; EGF_CA.
 CC InterPro; IPR006209; EGF_like.
 CC InterPro; IPR006605; GZF.
 CC InterPro; IPR000033; Ldl_receptor_rep.
 CC InterPro; IPR003886; Nidogen_ext.
 CC InterPro; IPR000716; Thyroglobulin_1.
 CC Pfam; PF00058; ldl_recept_bj_3.
 CC Pfam; PF00086; thyroglobulin_1; 1.
 CC SMART; SM00179; EGF_CA; 2.
 CC SMART; SM00682; GZF; 1.
 CC SMART; SM00135; LY; 5.

DR SMART; SM00539; NIDO: 1.
DR SMART; SM00211; TY: 1.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00484; THYROGLOBULIN_1; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 5.
DR PROSITE; PS01187; EGF_CA; 2.
KW Basement membrane; Extracellular matrix; Glycoprotein; Sulfation;
KW Signal; Calcium-binding; Repeat; EGF-like domain; Cell adhesion;
KM 3D structure. 1
FT SIGNAL 1 28
FT CHAIN 29 1247 NIDOGEN.
FT DOMAIN 29 669 I (LARGER GLOBULAR DOMAIN).
FT DOMAIN 917 1247 II (CYSTEINE-RICH).
FT DOMAIN 918 1247 III (SMALLER GLOBULAR DOMAIN).
FT DOMAIN 386 426 EGF-LIKE 1.
FT DOMAIN 668 709 EGF-LIKE 2.
FT DOMAIN 710 751 EGF-LIKE 3. CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 758 801 EGF-LIKE 4.
FT DOMAIN 802 840 EGF-LIKE 5. CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 872 919 THYROGLOBULIN TYPE I
FT DOMAIN 989 1030 LDI-RECEPTOR YWTD MOTIF 1.
FT DOMAIN 1032 1073 LDI-RECEPTOR YWTD MOTIF 2.
FT DOMAIN 1075 1118 LDI-RECEPTOR YWTD MOTIF 3.
FT DOMAIN 1124 1163 LDI-RECEPTOR YWTD MOTIF 4.
FT DOMAIN 1208 1244 EGF-LIKE 6.
FT MOD RES 289 289 SULFATION (POTENTIAL).
FT MOD RES 296 296 SULFATION (POTENTIAL).
FT MOD RES 672 685 BY SIMILARITY.
FT DISULFID 679 695 BY SIMILARITY.
FT DISULFID 697 708 BY SIMILARITY.
FT DISULFID 714 727 BY SIMILARITY.
FT DISULFID 721 736 BY SIMILARITY.
FT DISULFID 738 750 BY SIMILARITY.
FT DISULFID 762 777 BY SIMILARITY.
FT DISULFID 769 787 BY SIMILARITY.
FT DISULFID 789 800 BY SIMILARITY.
FT DISULFID 806 817 BY SIMILARITY.
FT DISULFID 811 826 BY SIMILARITY.
FT DISULFID 828 839 BY SIMILARITY.
FT DISULFID 1212 1223 BY SIMILARITY.
FT DISULFID 1219 1232 BY SIMILARITY.
FT DISULFID 1234 1243 BY SIMILARITY.
FT SITE 702 704 CELL ATTACHMENT SITE.
FT CARBOHYD 1137 1137 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 33 34 EL -> SS (IN REF. 2).
FT CONFLICT 37 42 FGRGOG -> SAPDR (IN REF. 2).
FT CONFLICT 115 115 H -> T (IN REF. 3).
FT SEQUENCE 1247 AA; 136488 MW; 46815B3CEC1575B CRC64;

Query Match 11.5%; Score 173.5; DB 1; Length 1247;
Best Local Similarity 25.8%; Pred. No. 6.6e-06;
Matches 80; Conservative 23; Mismatches 98; Indels 109; Gaps 18;

20 TEHAIVPPRRV-----CAVRAHG-----DPVSESFVQRYVQPLTTCGDGHRACSTYR 66
681 TNAACGPGFRTOFTGECISIGFRGDDGRTCYDIDEGSE-----QP--SVCGSHTICNNH- 730
67 TYRTAYRRSPGLAPARPRVYACCPGKRTSGRPGACGAIQCP--CRNG----- 114
731 -----DETFRCCEVEBEGQFSD--EGTVAVAVVDDRPINNYCETGIANCDIFQR 774
115 GSCVDPG-----RCRCPGAWRGD--TCQSDVDECSARRGCPORCINTAGSYWCQCEHGS 168
775 AQCITYTGSSSYTCSCLPGFSGGQACQ--DVDECSQSRGHPDAFCVNTGSGFTCCGCKPGY- 832
169 LSADGTLVCP-----KGGPRVAENPTG----- 191
833 -QGDFRRCVPEVEKTRCOHERENHILGAAGATDPPRPIRPGHVEPCDANGHVAPTCQHG 891
192 -----VDSAMKEEYORLOSRSVDLLEKQLQVLALPH-SLASQALEHGLDPRGSLVYHS 243
892 STGYCWCVDRDGR-EVEEGRIKRPCKMTPPCLSTVAAPPILHOGFVAVPTAIVLPLP-BGTHLL- 947

244 FQGLGRINDL 253
948 FAQTGRIERL 957

RESULT 15
PBL1_MOUSE
ID PBL1_MOUSE STANDARD; PRT; 2871 AA.
AC Q61554; Q60826;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibrillin-1 precursor.
GN PBL1 OR PBL-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95130561; PubMed=7829516;
RA Yin W., Gemmiller J., Sanguinetti C., Smiley E., Pangillman T.,
RA Pereira L., Ramirez F., Bonadio J.;
RT "Primary structure and developmental expression of Fbn-1, the mouse
fibrillin gene";
RL J. Biol. Chem. 270:1798-1806(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CD-1; TISSUE=Kidney;
RA Ota K., Kumar A., Mada J., Liu Z., Kanwar Y.S.;
RA Submitted (Apr-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS
THAT BINDS CALCIUM. FIBRILLIN-1-CONTAINING MICROFIBRILS
LONG-TERM FORCE BEARING STRUCTURAL SUPPORT.
CC -1- PTM: FORMS INTERMOLECULAR DISULFIDE BONDS EITHER WITH OTHER
FIBRILLIN-1 MOLECULES OR WITH OTHER COMPONENTS OF THE
MICROFIBRILS (BY SIMILARITY).
CC -1- SIMILARITY: Contains 47 EGF-like domains.
CC -1- SIMILARITY: Contains 7 TGF-beta binding protein (TGFBRP) domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL Outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L29454; AAA56840.1; -;
DR EMBL; U22493; AAA64217.1; -;
DR PIR; A55624; A55624.
DR HSSP; P35555; IABJ.
DR MGD; MGI:95489; Fbn1.
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR001881; EGF Ca.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR002212; Fibril-assoc.
DR Pfam; PF00008; EGF; 46.
DR Pfam; PF00683; TB; 9.
DR SMART; SM00179; EGF_CA; 42.
DR PROSITE; PS00010; ASX_HYDROXYL; 43.
DR PROSITE; PS00022; EGF_1; 2.
DR PROSITE; PS01186; EGF_2; 38.
DR PROSITE; PS01187; EGF_CA; 43.
KW Extracellular matrix; Calcium-binding; Glycoprotein; EGF-like domain;
KW Repeat; Signal; Multigene family.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 1 2871 FIBRILLIN 1.
FT DOMAIN 81 112 EGF-LIKE 1.
FT DOMAIN 115 146 EGF-LIKE 2.
FT DOMAIN 147 178 EGF-LIKE 3.
FT DOMAIN 246 287 EGF-LIKE 4. CALCIUM-BINDING.


```

Db      131 DHCLGQKGYIGH-----CGQPVCSGGCLNGGRCAVAPNRCACCTYGFTGQCBRDYRTGP 185
QY      136 -----S 136
Db      186 CFTVSNOMCGQLSGIVCTKTLCCATVGRAMGHPCEMCPAPHPGRGFIPNIRTAGCQ 245
QY      137 DVDECSARRGGCP-ORCINTAGSYWCQWEGHSLADGTL-----VPRGG----- 181
Db      246 DVDECOAIRFMCGGNCINTVGSFBCKCPAGHKFNESVSKCEDIDECSTIPGVCDGGSECT 305
QY      182 -----PPRVAPNPTG 191
Db      306 NTVSYYFCKCPGPGYTSPOG 325

```

Search completed: September 10, 2003, 17:13:31
 Job time : 25 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 10, 2003, 17:10:27; Search time 19 Seconds
(without alignments)
1381.792 Million cell updates/sec

Title: US-09-978-191a-506
Perfect score: 1505
Sequence: 1 MRGSOEVLIMMLVLA V G3T.....SEQISFLEEQLGSCSCCKKDS 273

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	435.5	28.9	293	T09065	hypothetical prote
2	256	17.0	1574	T13954	MEGF6 protein - ra
3	252.5	16.8	558	T1324	hypothetical prote
4	218	14.5	1620	T27283	hypothetical prote
5	196	13.0	1964	T09059	notch4 - mouse
6	189	12.6	678	B48089	growth arrest-spec
7	184	12.2	673	A48089	growth arrest-spec
8	183.5	12.2	2907	A57278	fibritillin-2 precur
9	180	12.0	810	T10756	Nel-homolog protei
10	178	11.8	674	I55476	growth potentiatin
11	176.5	11.7	3002	A47221	fibritillin 1 precur
12	175.5	11.7	2321	S78549	notch3 protein - h
13	174	11.6	835	JP0076	notch3 protein - h
14	173.5	11.5	1247	NMHUND	notch3 protein - h
15	173	11.5	2703	A24420	notch3 protein - h
16	172.5	11.5	2871	A55624	notch3 protein - h
17	172	11.4	2531	A46019	notch3 protein - h
18	171.5	11.4	2871	A55567	notch3 protein - h
19	170	11.3	675	1 KXMS	plasma protein S p
20	170	11.3	2918	2 A54105	fibritillin-2 precur
21	169.5	11.3	2318	2 S45306	notch3 protein - h
22	169	11.2	833	2 KXRTS	gene Delta protein
23	168	11.2	675	2 A31246	plasma protein S p
24	168	11.0	832	2 A31246	neurogenic protein
25	166	11.0	880	2 S00670	neurogenic repetit
26	164	10.9	1429	2 S06434	homoeoic protein 1
27	164	10.9	2524	2 A35844	Xorch protein - Af
28	164	10.9	3871	2 T22812	hypothetical prote
29	163.5	10.9	2555	2 A40043	notch protein homo

30	162	10.8	646	2	S38819	Plasma protein S -
31	161	10.7	387	2	B49175	Notch A protein -
32	161	10.7	675	1	KXBOS	Plasma protein S p
33	160.5	10.7	2531	2	S18188	notch protein homo
34	160	10.6	2437	2	S42612	transmembrane proc
35	158.5	10.5	407	1	KRBO7	coagulation factor
36	158.5	10.5	456	1	KXBO	protein C (activat
37	158	10.5	1820	2	A55494	latent transformin
38	157	10.4	676	1	KXHUS	plasma protein S p
39	156	10.4	642	2	S53434	plasma protein S p
40	156	10.4	1221	2	A49457	fibritillin-2 precuro
41	156	10.4	1408	2	S16148	gene serrate prote
42	155.5	10.3	466	1	KFHU7	coagulation factor
43	155.5	10.3	3635	2	T10053	laminin alpha 5 ch
44	155	10.3	2471	2	A49128	cell-fate determin
45	154	10.2	387	2	I38449	extracellular prot

ALIGNMENTS

RESULT 1
T09065
hypothetical protein - mouse
C/Species: Mus musculus (house mouse)
C/Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jan-2000
C/Accession: T09065
R/Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; Se
Submitted to the EMBL Data Library, October 1997
A/Description: Sequence of the mouse major histocompatibility locus class III region.
A/Reference number: Z16543
A/Accession: T09065
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-293 <R0W>
A/Cross-references: EMBL:AF030001; NID:G2564945; PID:G2564953
C/Genetics:
A/Map position: 17
A/Introns: 34/2; 75/2; 112/1; 144/1; 201/1; 228/3; 280/1
C/Superfamily: unassigned EGF-related proteins; EGF homology
F.114-141/Domain: EGF homology <EGF1>
F.148-183/Domain: EGF homology <EGF>

Query Match 28.9%; Score 435.5; DB 2; Length 293;
Best Local Similarity 37.3%; Pred. No. 8.9e-25;
Matches 112; Conservative 36; Mismatches 101; Indels 51; Gaps 14;

QY 1 MRGSOEVLIMMLVLA V G3T---HAYRGRVCAVRAHGDPV--SESFVQRFVQPFPLTTC 56
DB 11 LRG-----LSFVLVLMGEGTRGGSFKESLGVCSKQTLVPLRNVESVSGPVYKPYLTLC 65
QY 57 DGRHACSTYRTTYRYAVRSPGLAPARPRYAACCPCGKWRKTSGLPAACA-AICPPCRNGG 115
DB 66 AGRIRICSTYRTTYRYAVRSPGLAPARPRYAACCPCGKWRKTSGLPAACA-AICPPCRNGG 122
QY 116 SCVQPRGRCRCPAGKRGSPDTCGSDVDECSARGGCGQRICINTAAGSVCOCWESHSSADGTL 175
DB 123 VCTGPDRECAKPGGKGNCHVDVDECRASLTLTSHGCLNTLGSFLCSGPHLVLDGDR 182
QY 176 CVPKGPPRVAAPNPTGV-----DSAMKEEYVRLQSRVLDLEKIQLVLAFL 221
DB 183 CA--GGPE--SPTASISLVAVREADSEBERLRLRVEALRGRRLKLTG----- 228
QY 222 HSLASQ---LEHGLP-DPGSLVHSGQQL---GRIDSISEQISFLEBQLGSCSCCKKDS 273
DB 229 --WATQAGAWRAVLPMPPELREPEQVAVELWGRGDRITESISLSDQVLLLEBRIGACACBDNS 286

RESULT 2
T13954
MEGF6 protein - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000

Mol. Cell. Biol. 13, 4976-4985, 1993
A:Title: The protein encoded by a growth arrest-specific gene (gas6) is a new member of

A:Reference number: A48089; MUID:93330291; PMID:8336730

A:Accession: B48089
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-678 <MAN>

C:Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat hom

F:120-153/Domain: Gla domain homology #stratus atypical <Gla>

F:160-195/Domain: EGF homology <EG1>

F:201-236/Domain: EGF homology <EG2>

F:242-297/Domain: EGF homology <EG3>

F:311-671/Domain: sex hormone-binding globulin homology <SHB>

F:321-473/Domain: laminin G repeat homology <LGR>

Query Match 12.6%; Score 189; DB 2; Length 678;
Best Local Similarity 34.2%; Pred. No. 28-06;

Matches 53; Conservative 8; Mismatches 64; Indels 30; Gaps 8;

OY 46 QRVVOPFLTCDGH-----RACSTYRTIYRTRVRRSFGALPAPRYACC-----PGWK 93
Db 47 RRAPVDFEBAKQGHLERECEVERLCS--REAREVEVNDDETDYFYRYLIDCINKKGYSPYT 104

OY 94 RTSSG-----LRGCGAALICQPPC--RNGSGCVOP--GR--CRCPAGRRGDTCCQSDVDFPC 141
Db 105 KNISGATGCVQNLPPDQC---TNPFCDRKKTQACQDLMGFLCLCKAGWGRLLCDKXDVNVC 160

OY 142 SARRGCGPCRCINTAGSYWCQCMEGSHLSADGTLIC 176
Db 161 SQENGGCLQICHNKRGSPFHCSCGSEFELSSDRTIC 195

RESULT 7
A48089
G:Species: Mus musculus (house mouse)
C:Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 05-Nov-1999

C:Accession: A48089; S37437
R:Manifolietri, G.; Brancolini, C.; Avanzi, G.; Schneider, C.
Mol. Cell. Biol. 13, 4976-4985, 1993

A:Title: The protein encoded by a growth arrest-specific gene (gas6) is a new member of

A:Reference number: A48089; MUID:93330291; PMID:8336730

A:Accession: A48089
A:Status: preliminary
A:Molecule type: mRNA

A:Residues: 1-673 <MAN>

A:Cross-references: GB:X59846; NID:9407060; PIDN:GMA42507.1; PID:9407061

A:Note: authors translated the codon CCC for residue 424 as Ile

C:Genetics:

A:Gene: gas6

C:Superfamily: plasma protein S; EGF homology; Gla domain homology; laminin G repeat hom

F:38-89/Domain: Gla domain homology #stratus atypical <Gla>

F:117-150/Domain: EGF homology <EG1>

F:157-192/Domain: EGF homology <EG2>

F:198-233/Domain: EGF homology <EG3>

F:239-274/Domain: EGF homology <EG4>

F:308-666/Domain: sex hormone-binding globulin homology <SHB>

F:318-470/Domain: laminin G repeat homology <LGR>

Query Match 12.2%; Score 184; DB 2; Length 673;
Best Local Similarity 31.6%; Pred. No. 4.6e-06;

Matches 50; Conservative 8; Mismatches 64; Indels 36; Gaps 6;

OY 46 QRVVOPFLTCDGH-----RACSTYRTIYRTRVRRSFGALPAPRYACC----- 89
Db 44 RRAVDFEBAKQGHLERECEVERLCS--REAREVEVNDDETDYFYRYLIDCINKKGYSPYT 101
OY 90 --PGW-KRTSGLPAGC-----GAALCQPPCRNNGSGCVOPGRCPAGWRGDTCCQSDV 138

Db 102 KNPDFAKCVQNLPPDQC---TNPFCDRKKTQACQDLMGFLCLCKAGWGRLLCDKXDVNVC 154

OY 139 DECSARRGCGPCRCINTAGSYWCQCMEGSHLSADGTLIC 176

Db 155 NECVQKRGCGSDYCHNKRKGSFQCACHSGFSLASDQTC 192

RESULT 8
A57278
fibrillin-2 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 02-Aug-2002

C:Accession: A57278
R: Zhang, H.; Hu, W.; Ramirez, F.
J. Cell Biol. 129, 1165-1176, 1995

A:Title: Developmental expression of fibrillin gene suggests heterogeneity of extracell

A:Reference number: A57278; MUID:95263670; PMID:7744963

A:Accession: A57278
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-2907 <ZHA>

A:Cross-references: GB:I29790; NID:9762830; PIDN:AAA74908.1; PID:9762831

C:Superfamily: fibrillin I; EGF homology

F:1239-1274/Domain: EGF homology <EGF1>

F:2488-2523/Domain: EGF homology <EGF>

Query Match 12.2%; Score 183.5; DB 2; Length 2907;
Best Local Similarity 23.9%; Pred. No. 1.8e-05;

Matches 60; Conservative 19; Mismatches 85; Indels 87; Gaps 7;

OY 2 RGSQVLLMMLLVLAAGSTENHAY-----RPRRVCAVRAHGDVSEFVQVYQPFLL 54
Db 77 RGOQDEILNG---PNCVSGRPHSYCCPRGKWTLPBGNGQCLVPRICRNCGGGFCGR---PNNC 130

OY 55 TCDGHRACST--YRTIYRTRVRRSFGALPAPRYACCPRGWRKRTSGLPACGAAICQPPCR 112
Db 131 TCSSGQISPTGCRKSIQCCSVRCMNGTCTADDHCQCGKGYIGT-----YCGQPVENCGCQ 185

OY 113 NGSGCVOPGRCPRPGWRKRTSGLPACGAAICQPPCR 135
Db 186 NGRGCIIGNRCACVYGFPGPCERDRTGFCFTQVNNMCCGQLTGIVCTKTLCCATTGR 245

OY 136 -----SPVDECSARRGCGP--ORCINTAGSYWCQCME 165
Db 246 AMGHCEMCPAQPQPCRRGFIPIPIRTGACQVDVECAALPGLCCGGNCINTVSSFFCPCPA 305

OY 166 GHSLSADGTLIC 176
Db 306 GHKQSETTQKC 316

RESULT 9
T10756
Ncl-homolog protein - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C:Accession: T10756
R: Kuroda, S.; Tokunaga, C.; Kiyohara, Y.; Komishi, H.; Matsubashi, S.; Kikkawa, U.

submitted to the EMBL Data Library, November 1998

A:Description: Protein kinase C-binding protein.

A:Reference number: Z17122

A:Accession: T10756

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-810 <KUR>

A:Cross-references: EMBL:U48246; NID:93851179; PID:93851180

A:Experimental source: strain Sprague-Dawley, brain

Query Match 12.0%; Score 180; DB 2; Length 810;
Best Local Similarity 36.5%; Pred. No. 1.1e-05;

Matches 35; Conservative 13; Mismatches 38; Indels 10; Gaps 3;

OY 88 CCPGWRKRTSGLPAGC-----GAALCQPPCRNNGSGCVOPGRCPAGWRGDTCCQSDVDECSARRGG 147

DB 504 CQPGVYGN---GTTCKAKCEBECRGRGCVVAPNPKVCVCSGGFTGSHCEKDIDBCAEGFVE 559
 QY 148 CP--ORCINTAGSYWCQCBGH---SLGADGTLV 177
 DB 560 CHNYSRCVNLPGWYHCECRSGFHDDGTYSLSGESSCI 595

RESULT 10

153476 growth potentiating factor - rat
 C:Species: Rattus sp. (rat)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #next_change 20-Apr-2001
 A:Accession: I55476
 R:Nakano, T.; Higashino, K.; Kikuchi, N.; Kishino, J.; Nomura, K.; Fujita, H.; Ohara, O.
 J. Biol. Chem. 270, 5702-5705, 1995
 A:Title: Vascular smooth muscle cell-derived, Glu-containing growth-potentiating factor
 A:Reference number: I55476; MUID:95197586; PMID:7890695
 A:Accession: I55476
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 1-674 <RES>
 A:Cross-references: GB:D42148; NID:G1526567; PIDN:BA407719.1; PID:G9893402
 C:Superfamily: Plasma protein S; EGF homology; Glu domain homology; laminin G repeat hom
 F:29-89/Domain: Glu domain homology <GLA>
 F:117-150/Domain: EGF homology <EG1>
 F:157-192/Domain: EGF homology <EG2>
 F:198-233/Domain: EGF homology <EG3>
 F:239-274/Domain: EGF homology <EG4>
 F:308-647/Domain: sex hormone-binding globulin homology <SHB>
 F:318-470/Domain: laminin G repeat homology <LGR>

Query Match 11.8%; Score 178; DB 2; Length 674;
 Best Local Similarity 30.4%; Pred. No. 1.3e-05;
 Matches 48; Conservative 8; Mismatches 66; Indels 36; Gaps 6;

QY 46 QRYVQPLTCDGH-----RACSTYRTYPTAYRSGLAPRPRVACC----- 89
 DB 44 RRAYVFEBAKQGHLEBCEVCSKEA--KEVFENDEDTDYFRYVQCRKXGRPEP 101
 QY 90 --PQWR-TSGLPAGC-----GAITQPPCRNGSCVQPRCPCPAWGRDTCQSDV 138
 DB 102 KNPVNFATCVKNLPDQCTPNPCKKGTQLQODLWGN-----FFCLCKDQWGGRLCDKDV 154
 QY 139 DECSARGGGCPORCINTAGSYWCQCBGHSLGADGTLG 176
 DB 155 NECSQKMGCSQVCHNKPGSPQACHSGFSLQSDNKS 192

RESULT 11
 A47221 fibrillin 1 precursor - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 02-Jun-1995 #sequence_revision 25-Apr-1997 #next_change 02-Aug-2002
 C:Accession: A47221; I54355; S17064; S17062; S62111; A34198
 R:Corson, G.M.; Chalberg, S.C.; Dietz, H.C.; Charbonneau, N.L.; Sakai, L.Y.
 Genomics 17, 476-484, 1993
 A:Title: Fibrillin binds calcium and is coded by cDNAs that reveal a multidomain structure
 A:Reference number: A47221; MUID:94010947; PMID:7691719
 A:Accession: A47221
 A:Molecule type: mRNA
 A:Residues: 1-337; 'T', 339-1029 <COR>
 A:Cross-references: GB:X63556
 R:Perleza, L.V.; D'Alessio, M.; Ramirez, F.; Lynch, J.; Sykes, B.; Panglman, T.; Bonad
 Hum. Mol. Genet. 2, 961-968, 1993
 A:Title: Genomic organization of the sequence coding for fibrillin, the defective gene F
 A:Reference number: I54355; MUID:93372860; PMID:8364578
 A:Accession: I54355
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: mRNA
 A:Residues: 132-3002 <PER>
 A:Cross-references: GB:L13923; NID:G306745; PIDN:AAB02036.1; PID:G306746
 R:Maslen, C.L.; Corson, G.M.; Maddox, B.K.; Glanville, R.W.; Sakai, L.Y.

Nature 352, 334-337, 1991
 A:Title: Partial sequence of a candidate gene for the Marfan syndrome.
 A:Reference number: S17064; MUID:91304568; PMID:1852207
 A:Accession: S17064
 A:Molecule type: mRNA
 A:Residues: 1030-3002 <MAS>
 A:Cross-references: EMBL:X63556
 R:Dietz, H.C.; Valle, D.; Francomano, C.A.; Kendzior, R.J.
 Science 259, 680-683, 1993
 A:Title: The skipping of constitutive exons in vivo induced by nonsense mutations.
 A:Reference number: I59574; MUID:93157831; PMID:8430317
 A:Accession: I59574
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 2217-2288; 'T', 2290-2325 <RES>
 A:Cross-references: GB:S54426; NID:G264860; PIDN:AAB25244.1; PID:G264861
 R:Lee, B.; Godfrey, M.; Valcalle, E.; Holt, H.; Matter, M.G.; Sarlatzki, M.; Tsipouras, P.
 Nature 352, 330-334, 1991
 A:Title: Linkage of Marfan syndrome and a phenotypically related disorder to two differe
 A:Reference number: S17062; MUID:91304567; PMID:1852206
 A:Accession: S17062
 A:Molecule type: mRNA
 A:Residues: 'LVTVVFILSYVKML', 944-1444 <LEB1>
 A:Cross-references: EMBL:X62008; NID:G31398; PIDN:CAB56534.1; PID:G95924015
 A:Accession: S62111
 A:Molecule type: protein
 A:Residues: 1166-1176; 'X', 1178-1180; 'D', 1182-1185 <LEB2>
 R:Maddox, B.K.; Sakai, L.Y.; Keene, D.R.; Glanville, R.W.
 J. Biol. Chem. 264, 21381-21385, 1989
 A:Title: Connective tissue microfibrils. Isolation and characterization of three large p
 A:Reference number: A34198; MUID:90078246; PMID:2512293
 A:Accession: A34198
 A:Molecule type: protein
 A:Residues: 565-575; 1890-1892; 'T', 1894-1900 <MAD>
 C:Comment: Fibrillin is a major component of elastin-associated microfibrils.
 C:Genetics:
 A:Gene: GDB:FBNI
 A:Cross-references: GDB:127115; OMI:134797; OMI:154700
 A:Map position: 15q21.1-15q21.1
 A:Introns: 2236/1, 2258/1; 2297/1
 C:Superfamily: Fibrillin 1; EGF homology
 C:Keywords: alternative splicing; calcium binding; extracellular matrix; glycoprotein; I
 F:1-3002/Product: fibrillin (5'-region exon A splice form) (fragment) #status predicted
 F:132-3002/Product: fibrillin (5'-region exon C splice form) #status predicted <MATC>
 F:133-1367/Domain: EGF homology <EGF>
 F:1457-1492/Domain: EGF homology <EGF2>
 F:2262-2295/Domain: EGF homology <EGF1>

Query Match 11.7%; Score 176.5; DB 2; Length 3002;
 Best Local Similarity 22.7%; Pred. No. 6e-05;
 Matches 59; Conservative 19; Mismatches 79; Indels 103; Gaps 8;

QY 26 PRRVCAVRAHGDPPSEFVQRYVQPLTCDGH--ACSTYRTYPTAYRSGLAPA 82
 DB 206 PEGNOCIVPICRHSGDGFCSG---PNNCTPSSGDIADSCS-RIOHCNIRCMNGSSCS 261
 QY 83 RPRVACCPGKWRKTSGLPAGCAIQCPCRRNGSCVQPRCPCPAWGRDTCQSDV 135
 DB 262 DDHCLCQKXGTYGTH-----CGQPVESGLANGRCVAPARACACTYGFPGPCERDRTGP 316
 QY 136 -----S 136
 DB 317 CFTVINSQMGQGLSIVYCTKQLCCATVGRAMGHCPCMAQPHRCRRGFTPIRITGACQ 376
 QY 137 DVDEGSARRGGCP-ORCINTAGSYWCQCBGHSLGADGTLG-----VPRGG--- 181
 DB 377 DVDECAIIFGICOGGANCTNTVGSFECPCPAWGRDTCQSDV-----VPRGG--- 436
 QY 182 -----PPRVANPTG 191
 DB 437 NTVSSYFCKCPGFRYTSFDG 456

RESULT 12

S78549 notch3 protein - human
 C:Species: Homo sapiens (man)
 C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 08-Sep-2002
 C:Accession: S78549; S71825
 R:Joutel, A.; Tournier-Lasserre, E. submitted to the EMBL Data Library, April 1997
 A:Reference number: S78549
 A:Accession: S78549
 A:Molecule type: mRNA
 A:Residues: 1-2321 <JOU1>
 A:Cross-references: EMBL:097669; NID:92668591; PIDN:AAB91371.1; PID:92668592
 R:Joutel, A.; Corpechot, C.; Ducros, A.; Vahedi, K.; Chabrialat, H.; Mouton, P.; Alamowitz, M.M.; Weissenbach, J.; Bach, J.F.; Bousselet, M.G.; Tournier-Lasserre, E. Nature 383, 707-710, 1996
 A>Title: Notch3 mutations in CADASIL, a hereditary adult-onset condition causing stroke
 A:Reference number: S71825; MUID:97032728; PMID:8878478
 A:Accession: S71825
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 67-113;138-194;268-333; 'G', 335-346;536-613;716-765;1240-1279;1815-1888 <JOU2
 A:Cross-references: EMBL:097669
 C:Genetics: notch3
 A:Map position: 19p13.1
 C:Function:
 A:Description: may be involved in pathogenesis of CADASIL, causing a type of stroke and
 C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
 C:Keywords: tandem repeat; transmembrane protein
 F:123-155/Domain: EGF homology <EGX1>
 F:162-194/Domain: EGF homology <EGF1>
 F:240-271/Domain: EGF homology <EGX2>
 F:318-349/Domain: EGF homology <EGF2>
 F:473-504/Domain: EGF homology <EGF3>
 F:853-884/Domain: EGF homology <EGF3>
 F:928-959/Domain: EGF homology <EGX4>
 F:1838-1870/Domain: ankyrin repeat homology <AN1>
 F:1871-1903/Domain: ankyrin repeat homology <AN2>
 F:1905-1937/Domain: ankyrin repeat homology <AN3>
 F:1938-1970/Domain: ankyrin repeat homology <AN4>
 F:1971-2003/Domain: ankyrin repeat homology <AN5>

Query Match 11.7%; Score 175.5; DB 2; Length 2321;
 Best Local Similarity 34.5%; Pred. No. 57e-05;
 Matches 50; Conservative 14; Mismatches 44; Indels 37; Gaps 11;

Oy 56 CDGHRACSTYRTTYRTRAVYRRSPGLAPARPRVAC-CPGWKR--TSGLPAGCAAIQCPPCR 112
 Db 87 CAGRGVCCS-----SVVAAGTARAFRCRCRCPGRGPDGSLDPDC-----LSSPCA 129
 Oy 113 NGGSC-VQP-GR-CRCPAGMFGDTCQSPVDEC-----SARRGCGRCICINTAGSYWCCGW 164
 Db 130 HGARSVSPDGGFLCSCPGGRSRSVDCRVEBPCRHGG---TCINTPGRSFRCCCP 186
 Oy 165 EGHSLADGTLCPVKGKGGPRVAVPNP 189
 Db 187 AGYT---GFLCENPVP--CAPSP 205

RESULT 13

JF0076 nel protein - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 24-Feb-1995 #sequence_revision 24-Feb-1995 #text_change 13-Aug-1999
 C:Accession: A38963; JP0076
 R:Matsumashi, S.; Noji, S.; Koyama, E.; Myokai, F.; Ohuchi, H.; Taniguchi, S.; Horii, K. Dev. Dyn. 203, 212-222, 1995
 A>Title: New gene, nel, encoding a Mr 93k protein with EGF-like repeats is strongly expressed in the developing chick
 A:Reference number: A38963; MUID:95383734; PMID:7655083
 A:Accession: A38963
 A:Molecule type: mRNA
 A:Residues: 1-835 <MAT>

A:Cross-references: DDBJ:D45365
 A:Experimental source: 9-day embryo
 R:Matsumashi, S.; Noji, S.; Koyama, E.; Myokai, F.; Ohuchi, H.; Taniguchi, S.; Horii, K. submitted to JPIID, January 1995
 A:Description: A new gene, nel, encoding a Mr 93k protein with EGF-like repeats is strongly expressed in the developing chick
 A:Reference number: JP0076
 A:Accession: JP0076
 A:Molecule type: mRNA
 A:Residues: 1-835 <MA2>
 A:Cross-references: DDBJ:D45365
 A:Experimental source: 9-day embryo
 C:Superfamily: von Willebrand factor type C repeat homology; EGF homology
 F:273-333/Domain: von Willebrand factor type C repeat homology <WVC>
 F:395-592/Region: EGF-like repeats
 F:444-480/Domain: EGF homology <EGF1>
 F:486-521/Domain: EGF homology <EGF-
 F:525-552/Domain: EGF homology <EGF2>

Query Match 11.6%; Score 174; DB 2; Length 835;
 Best Local Similarity 42.9%; Pred. No. 3e-05;
 Matches 30; Conservative 11; Mismatches 27; Indels 2; Gaps 1;

Oy 100 GACGAIICQPPCRNGSCVQPERCRCPAGMFGDTCQSPVDECSSARRGCGCPOR-CINTAG 157
 Db 518 GTVCKAFCKDGGCRMGACIASNVVCACPGGFTGSPSCETIDICSDGFPVCDSRANCIIDPFG 577
 Oy 158 SYWCCWEGH 167
 Db 578 WHCRCRDGY 587

RESULT 14

MMHUND nidogen precursor - human
 N:Alternate names: entactin
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 20-Oct-2000
 C:Accession: A33322; A32437; A61367
 R:Nagayoshi, T.; Sanborn, D.; Hickok, N.J.; Olsen, D.R.; Fazio, M.J.; Chu, M.L.; Knowlton, D.N. J. Biol. Chem. 266, 591-594, 1991
 A>Title: Human nidogen: complete amino acid sequence and structural domains deduced from complementary DNA
 A:Reference number: A33322; MUID:90091745; PMID:2574658
 A:Accession: A33322
 A:Molecule type: mRNA
 A:Residues: 1-1247 <NAG>
 A:Cross-references: EMBL:M30269
 R:Olsen, D.R.; Nagayoshi, T.; Fazio, M.; Matrei, M.G.; Passage, E.; Well, D.; Timpl, R.; Am. J. Hum. Genet. 44, 876-885, 1989
 A>Title: Human nidogen: cDNA cloning, cellular expression, and mapping of the gene to chromosome 10
 A:Reference number: A32437; MUID:89270475; PMID:2471408
 A:Accession: A32437
 A:Molecule type: mRNA
 A:Residues: 667-1247 <OLS>
 A:Cross-references: EMBL:M27445; NID:9602466; PIDN:AAA57261.1; PID:9602467
 A>Note: the authors translated the codon AAG for residue 966 as Cys
 R:Fazio, M.J.; O'Leary, J.; Kaehnerl, V.M.; Chen, Y.Q.; Salter, B.; Vitro, J. J. Invest. Dermatol. 97, 281-285, 1991
 A>Title: Human nidogen gene: structural and functional characterization of the 5'-flanking region
 A:Reference number: A61367; MUID:91302882; PMID:1906509
 A:Accession: A61367
 A:Molecule type: DNA
 A:Residues: 1-28 <FAZ>
 A:Comment: This protein is a basement membrane glycoprotein that forms a complex with laminin and nidogen.
 C:Genetics: GDB:NID
 A:Gene: GDB:NID
 A:Cross-references: GDB:120236; OMTM:131390
 A:Map position: 14q31-q43
 C:Superfamily: nidogen; EGF homology; LDL receptor YWTD-containing repeat homology; thyr C:Keywords: basement membrane; beta-hydroxyaspartagine; calcium binding; cell binding; collagen binding
 F:1-28/Domain: signal sequence #status predicted <SIG>
 F:129-1247/Product: nidogen #status predicted <MAT>
 F:390-425/Domain: EGF homology <EG1>

F:672-708/Domain: EGF homology <EG2>
 F:1702-704/Region: cell attachment (R-G-D) motif
 F:114-750/Domain: EGF homology <EG3>
 F:762-800/Domain: EGF homology <EG4>
 F:806-839/Domain: EGF homology <EG5>
 F:849-919/Domain: thyroglobulin type I repeat homology <THY1>
 F:990-1033/Domain: LDL receptor WYTD-containing repeat homology <YW1>
 F:1033-1075/Domain: LDL receptor WYTD-containing repeat homology <YW2>
 F:1076-1120/Domain: LDL receptor WYTD-containing repeat homology <YW3>
 F:1121-1160/Domain: LDL receptor WYTD-containing repeat homology <YW4>
 F:1161-1197/Domain: LDL receptor WYTD-containing repeat homology <YW5>
 F:1212-1243/Domain: EGF homology <EG6>
 F:289-296/Binding site: sulfate (TYR) (covalent) #status predicted
 F:129-819/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
 F:756/Cross-link: isopeptide (Gln) (interchain to Lys N6-amino of laminin) #status predi
 F:1137/Binding site: carbonylate (Asn) (covalent) #status predicted

Query Match 11.5%; Score 173.5; DB 1; Length 1247;
 Best Local Similarity 25.8%; Pred. No. 4.6e-05;
 Matches 80; Conservative 23; Mismatches 98; Indels 109; Gaps 18;

QY 20 TEHAHPGRRV-----CAVRAG-----DPVSESPVQRYVQPLTTCDGHRACSTYR 66
 Db 681 TNAAACRPGRPTQPTCECSIGFRDGRGRTCYDIDECSE-----QP--SYGSHHTCNMH- 730
 QY 67 TYRTAYRRSPGLAPARPRYACCPGKMRITSGLPAGCAAIICPP-----CRNG----- 114
 Db 731 -----PSTFRCEVVEGQFSD--EGTVAVAVDDEPPIVYCTGLHNCIDIPOR 774
 QY 115 GSCVDPG---RRCPCPAGNRD--TQSDVDECSARRGGCPORCINTAGSYWCQCEWEGHS 168
 Db 775 AQCIVYGGSSYTCSCIPGFSGGDQACQ-DVDECGPQRCHPDACVYVTPGSPFCQCKPQY- 832
 QY 169 LSADGTLCTP-----KGGPRVAVPNTG----- 191
 Db 833 -GGDGRVCVPEVEKTRCQHERENHIGAAAGVNDPQRPPIPGLVPEPCDAHGHVAPYQCHG 891
 QY 192 -----VDSAMKEEYQRIQRVLDLEKIQLVIAFLH-SLAAQALEHGLPDPGSLVYHS 243
 Db 892 STGTCYKCVDRDGR-EVEGRTIRPGMTPPCLSTYVAPFHGGPAPVAVIPLP-PGTHLL-- 947
 QY 244 FOOLGRIDSL 253
 Db 948 PAQTGKIERL 957

RESULT 15
 A24420
 notch protein - fruit fly (Drosophila melanogaster)
 N:Alternate names: neurogenic repetitive locus protein
 C:Species: Drosophila melanogaster
 C>Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #ext_change 10-Sep-1999
 C:Accession: A24420; A24768; S09358; A05267
 R:Kidd, S.; Kelley, M.R.; Young, M.W.
 MOl. Biol. 6, 3094-3108, 1986
 A:Reference number: A24420; WUID:87064624; PMID:3097517
 A:Accession: A24420
 A:Molecule type: DNA
 A:Residues: 1-2703 <KID>
 A:Cross-references: GB:K03508; NID:G157991; PIDN:AAA28725.1; PID:G157993
 R:Wharton, K.A.; Johansen, K.M.; Xu, T.; Aravanis-Teakonas, S.
 Cell 43, 567-581, 1985
 A:Reference number: A24768; WUID:86079539; PMID:3935325
 A:Accession: A24768
 A:Molecule type: mRNA
 A:Residues: 1-48, '1', 50-118, 'R', 120-230, '1', 232-256, 'N', 258-266, 'A', 268-872, 'R', 874-958,
 A:Note: The authors translated the codon ATC for residue 49 as Thr, ATT for residue 2044
 R:Tautz, D.
 Nucleic Acids Res. 17, 6463-6471, 1989
 A:Title: Hypervariability of simple sequences as a general source for polymorphic DNA ma
 A:Reference number: S09358; WUID:89585974; PMID:2780284
 A:Accession: S09358
 A:Molecule type: DNA

A:Residues: 2505-2551, '0000', 2552-2576, 'E', 2578-2604 <TMU>
 R:Wharton, K.A.; Yedvobnick, B.; Finerty, V.G.; Aravanis-Teakonas, S.
 Cell 40, 55-62, 1985
 A:Title: opa a novel family of transcribed repeats shared by the Notch locus and other
 A:Reference number: A05267; WUID:85099329; PMID:2981631
 A:Accession: A05267
 A:Molecule type: DNA
 A:Residues: 2504-2576, 'E', 2578-2611 <WHA2>
 C:Genetics:
 A:Gene: notch; opa
 A:Cross-references: FlyBase:FBgn0004647
 A:Map position: 8.96-9.36
 A:Introns: 53/3; 84/3; 171/3; 240/3; 283/3; 2333/3; 2436/3; 2588/3
 C:Superfamily: notch protein; ankyrin repeat homology; EGF homology
 C:Keywords: differentiation; tandem repeat; transmembrane protein
 F:27-43/Domain: transmembrane #status predicted <TM1>
 F:297-328/Domain: EGF homology <EGX1>
 F:530-561/Domain: EGF homology <EGF1>
 F:568-599/Domain: EGF homology <EGF>
 F:988-1019/Domain: EGF homology <EGX2>
 F:1064-1095/Domain: EGF homology <EGF3>
 F:1187-1218/Domain: EGF homology <EGX3>
 F:11746-1162/Domain: transmembrane #status predicted <TM2>
 F:1950-1982/Domain: ankyrin repeat homology <AN1>
 F:1983-2015/Domain: ankyrin repeat homology <AN2>
 F:1988-2004/Domain: transmembrane #status predicted <TM3>
 F:2017-2049/Domain: ankyrin repeat homology <AN3>
 F:2050-2082/Domain: ankyrin repeat homology <AN4>
 F:2083-2115/Domain: ankyrin repeat homology <AN5>
 F:2538-2568/Region: glutamine-rich
 F:2538-2568/Domain: neurogenic repetitive element #status predicted <OPA>

Query Match 11.5%; Score 173; DB 1; Length 2703;
 Best Local Similarity 26.7%; Pred. No. 9.9e-05;
 Matches 59; Conservative 19; Mismatches 67; Indels 76; Gaps 13;

QY 18 GTEHAHYPPGRVCAVRAH--GDPVSESPVQRYVQPLTTCDGHRACSTYRTIYRTAYR 75
 Db 70 GGTCTQIANGKTYTACDSHYVD-----YCEHNPQNSMR--QNGGTQVTFPANG 118
 QY 76 SPGLAPARPRYAC-CP-GWKRT--SGLPAGCAAIIC----- 107
 Db 119 HPGI-----SKCEPLDFDESLEIHAVPNAACDHVTCINGSTCOLKLEEYTCACANGYT 171
 QY 108 -----QPPRNGSGV-----QPRGRCPCPAGNRGPTQSDVDECSA---RRGCC 148
 Db 172 GERCTKNLCASSPERRNATCTALAGSSSFTSCSPGFTGDTCSYDIBECQSNPKYGG- 230
 QY 149 PORCINTAGSYWCQCEWEGHSLSADGTLCTVPRKGPVAVP 189
 Db 231 --TCVNTHTGSIYQCMCPGTG---GXDDDTKYKP--CSPSP 263

Search completed: September 10, 2003, 17:15:38
 Job time : 21 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 10, 2003, 17:13:38 ; Search time 21 Seconds
(without alignments)
267.752 Million cell updates/sec

Title: US-09-978-191A-506

Perfect score: 1505 1 MRGSEQVLLMVLVAVGVT.....SEQISFLEEQIGSCCKKDS 273

Sequence: 1 MRGSEQVLLMVLVAVGVT.....SEQISFLEEQIGSCCKKDS 273

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87302 seqs, 20596313 residues

Total number of hits satisfying chosen parameters: 87302

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

*Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1504	99.9	285	US-10-425-114A-37265	Sequence 37265, A
2	251.5	16.7	436	US-60-487-610-1532	Sequence 1532, Ap
3	251.5	16.7	553	US-60-487-610-1530	Sequence 1530, Ap
4	251.5	16.7	565	US-60-487-610-1531	Sequence 1531, Ap
5	223	14.8	509	US-09-908-576-315	Sequence 315, App
6	188.5	12.5	2003	US-60-487-610-1823	Sequence 1823, Ap
7	182	12.1	810	PCT-US02-29560A-361	Sequence 361, App
8	181	12.0	366	PCT-US03-25418-41	Sequence 41, Appl
9	176.5	11.7	393	PCT-US03-25418-3	Sequence 3, Appl
10	176.5	11.7	2871	US-60-490-890-481	Sequence 481, App
11	176	11.7	1587	US-60-487-610-1941	Sequence 1941, Ap
12	175.5	11.7	2321	US-60-487-610-2570	Sequence 2570, Ap
13	175	11.6	671	US-60-485-450-1335	Sequence 1335, Ap
14	173.5	11.5	1247	US-60-487-610-2260	Sequence 2260, Ap
15	168.5	11.2	604	PCT-US02-24483-4	Sequence 4, Appl
16	168.5	10.9	1631	US-60-487-610-1861	Sequence 1861, Ap
17	163.5	10.9	2556	US-10-294-006-12	Sequence 12, Appl
18	160.5	10.7	618	PCT-US02-29560A-301	Sequence 301, App
19	158.5	10.5	467	PCT-US02-24483-176	Sequence 176, App
20	158.5	10.5	1435	US-60-487-610-1817	Sequence 54, Appl
21	158	10.5	1821	US-60-485-450-1179	Sequence 1817, Ap
22	158	10.5	1821	US-60-485-450-1179	Sequence 1179, Ap
23	156	10.4	999	US-09-976-858-189	Sequence 189, App
24	155.5	10.3	481	US-60-495-114-1951	Sequence 1951, Ap
25	155.5	10.3	481	US-60-495-114-1952	Sequence 1952, Ap
26	155.5	10.3	481	US-60-495-135-406	Sequence 406, App

27	155.5	10.3	481	7	US-60-495-135-407	Sequence 407, App
28	155	10.3	630	1	PCT-US02-24483-2	Sequence 2, Appl
29	154	10.2	874	6	US-10-294-006-34	Sequence 34, Appl
30	153	10.2	1218	6	US-10-648-593-155	Sequence 155, App
31	151	10.0	524	1	PCT-US03-24084-2	Sequence 2, App
32	151	10.0	1799	7	US-60-485-450-1228	Sequence 1228, Ap
33	151	10.0	1905	1	PCT-US02-05093-6	Sequence 6, App
34	150	10.0	495	7	US-60-495-114-1953	Sequence 1953, Ap
35	150	10.0	459	7	US-60-495-114-1954	Sequence 1954, Ap
36	150	10.0	459	7	US-60-495-135-408	Sequence 408, App
37	150	10.0	459	7	US-60-495-135-409	Sequence 409, App
38	148	9.8	379	5	US-09-908-576-4	Sequence 4, App
39	148	9.8	1185	7	US-60-485-450-1176	Sequence 1176, Ap
40	147	9.8	1184	1	PCT-US02-38594-6	Sequence 6, App
41	146	9.7	2225	7	US-60-487-610-2532	Sequence 2532, Ap
42	145	9.6	986	7	US-60-487-610-2032	Sequence 2032, Ap
43	145	9.6	1132	7	US-60-487-610-2033	Sequence 2033, Ap
44	144.5	9.6	461	7	US-60-495-114-1137	Sequence 1137, Ap
45	144.5	9.6	461	7	US-60-495-135-264	Sequence 264, App

ALIGNMENTS

```

RESULT 1
US-10-425-114A-37265
; Sequence 37265, Application US/10425114A
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongqei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425, 114A
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 37265
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB43-95-B8_FL1.pep
US-10-425-114A-37265
Query Match          99.9%; Score 1504; DB 6; Length 285;
Best Local Similarity 99.6%; Pred. No. 1.7e-108;
Matches 272; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
1 MRGSEQVLLMVLVAVGTEHAYRPGRRVCAVBAHGDVSESFVQRYVYQPLFTTCGHR 60
13 MRGSEQVLLMVLVAVGTEHAYRPGRRVCAVBAHGDVSESFVQRYVYQPLFTTCGHR 72
61 ACSTYRTTYRATYRSPGLAPARPRVYACCPGKRTSGIPGACGAITCOPPRNGSCVQP 120
73 ACSYRTTYRATYRSPGLAPARPRVYACCPGKRTSGIPGACGAITCOPPRNGSCVQP 132
121 GRCCPAGMRGDTQOSVDVDECSARGGCPQRCVNTTASGYMCQCEGHSLSADGTLCPVK 180
133 GRCCPAGMRGDTQOSVDVDECSARGGCPQRCVNTTASGYMCQCEGHSLSADGTLCPVK 192
181 GPPVAVPPTGVDSAMKEEVORLQSRVLDLBEKQLVLIAPLHSLASQALEHGLDPPGSL 240
193 GPPVAVPPTGVDSAMKEEVORLQSRVLDLBEKQLVLIAPLHSLASQALEHGLDPPGSL 252
241 VHSFOQGRIDLSSEQISFLEEQIGSCCKKDS 273
253 VHSFOQGRIDLSSEQISFLEEQIGSCCKKDS 285

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; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143, 048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145, 698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146, 222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; Remaining Prior Application data removed - See file Wrapper or PALM.
; SEQ ID NO 315
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-908-576-315

```

```

Query Match
Best Local Similarity 42.4%; Score 223; DB 5; Length 509;
Matches 42; Conservative 13; Mismatches 40; Indels 4; Gaps 3;

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QY 76 SFGIAPAPRYAACPCGKRTSGLPAGCAAIICQPPCRNGSCVOPGRCRCPAGWRGDTQC 135
Db 32 SGLGRYGRIRIDCCGMARQSN--GQC-QPVCQPRCKH-GEICIGNKCKCHGYAKTKCN 87
QY 136 SDVDECSARRGGCCPQRCINTAGSYWCQCEGHSLSADGT 174
Db 88 QDINECGKPRPCRKRCMNTYGSYKCYCIANGYMLMPDGS 126

```

```

RESULT 6
US-60-487-610-1823
; Sequence 1823, Application US/60487610
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
; FILE REFERENCE: CLO01469
; CURRENT APPLICATION NUMBER: US/60/487, 610
; NUMBER OF SEQ ID NOS: 97101
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1823
; LENGTH: 2003
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-487-610-1823

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```

Query Match
Best Local Similarity 12.5%; Score 188.5; DB 7; Length 2003;
Matches 61; Conservative 17; Mismatches 87; Indels 41; Gaps 11;

```

```

QY 80 APAPRYAACPCGKRTSGLPAGCAAIICQPPCRNGSCVOPG--RRCRPAWRGDTQC 135
Db 137 ASGRPOCCSMGEMTGECCQLRDFCSA---NPCVNGVCLATVYPOIQCHCPGFEHACE 192
QY 136 SDVDECSARRGGCCPQRCINTAGSYWCQCEGHSLSADGTLCVYKGG--PRAVAPRPTG 191
Db 193 RDVNECFDDPGFCRGTSGHNTLSFQCLCPVQ---BGRCELRAPGCPRRGCSN--GG 247
QY 192 VDSAKKEEVORLQSRVLDLLEKQLVLAFLHSLASQALEHGLPD---PGSLLVHSPQOL 247

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Db 248 TCOLMPEK-----DSTFHLCLCPPEFG-----PDCVNPBNCVSHQCCNG 288
QY 248 GRI-DLSLSEQISFLBEQJGSCSCCKKD 272
Db 289 GTCCQDGLDPTTCLCPETWTGWDCESD 314

```

```

RESULT 7
PCT-US02-29560A-361
; Sequence 361, Application PC/TUS0229560A
; GENERAL INFORMATION:
; APPLICANT: Afari, Daniel
; APPLICANT: Aziz, Natasha
; APPLICANT: Gish, Kurt C.
; APPLICANT: Hevezi, Peter A.
; APPLICANT: Mack, David H. E.
; APPLICANT: Wilson, Keith E.
; APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
; FILE REFERENCE: 018501-002710PC
; CURRENT FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: PCT/US02/29560A
; PRIOR FILING DATE: 2001-09-17
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 361
; LENGTH: 810
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-29560A-361

```

```

Query Match
Best Local Similarity 12.1%; Score 182; DB 1; Length 810;
Matches 36; Conservative 12; Mismatches 38; Indels 10; Gaps 3;

```

```

QY 88 CTCRWRKRTSGLPAGCAAAICQPPCRNGSCVOPGRCRCPAGWRGDTQCSVDVDECSARRGG 147
Db 504 CKPVGYN---GTCRFRFCBEGCRYGTCVAPMKCVCPSPGFTSHCKEDIDECSEGIIE 559
QY 148 C--PQRCINTAGSYWCQCEGHSLSADGTLCV 177
Db 560 CHNHRVCVNLPMGWYHCBGRSGFPHDDGTYSLSGSECI 595

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```

RESULT 8
PCT-US03-25418-41
; Sequence 41, Application PC/TUS0325418
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION
; APPLICANT: ELIOTT, Vicki S.
; APPLICANT: KHARE, Reena
; APPLICANT: EMERLING, Brooke M.
; APPLICANT: KABLE, Amy E.
; APPLICANT: TRAN, Uyen K.
; APPLICANT: JIN, Pei
; APPLICANT: BECHA, Shanya D.
; APPLICANT: MARQUIS, Joseph P.
; APPLICANT: SWARNAKAR, Anita
; APPLICANT: SHAWLA, Narinder K.
; APPLICANT: RAMKUMAR, Jayalaxmi
; APPLICANT: HAFALIA, April J.A.
; APPLICANT: LEE, Soo Yeun
; APPLICANT: JIANG, Xin
; APPLICANT: JACKSON, Alan A.
; APPLICANT: RICHARDSON, Thomas W.
; APPLICANT: BLAKE, Julie J.
; APPLICANT: WANG, Jonathan T.
; APPLICANT: CHIEN, David
; APPLICANT: YANG, Yonghong G.

```

```

/ TITLE OF INVENTION: CELL ADHESION AND EXTRACELLULAR MATRIX PROTEINS
/ FILE REFERENCE: PR-1500 PCT
/ CURRENT APPLICATION NUMBER: PCT/US03/25418
/ CURRENT FILING DATE: 2003-08-12
/ PRIOR APPLICATION NUMBER: US 60/403,781
/ PRIOR FILING DATE: 2002-08-13
/ PRIOR APPLICATION NUMBER: US 60/407,034
/ PRIOR FILING DATE: 2002-08-30
/ PRIOR APPLICATION NUMBER: US 60/410,566
/ PRIOR FILING DATE: 2002-09-13
/ PRIOR APPLICATION NUMBER: US 60/413,482
/ PRIOR FILING DATE: 2002-09-24
/ PRIOR APPLICATION NUMBER: US 60/413,890
/ PRIOR FILING DATE: 2002-09-25
/ PRIOR APPLICATION NUMBER: US 60/424,904
/ PRIOR FILING DATE: 2002-11-08
/ PRIOR APPLICATION NUMBER: US 60/426,222
/ PRIOR FILING DATE: 2002-11-13
/ NUMBER OF SEQ ID NOS: 84
/ SOFTWARE: PERL Program
/ SEQ ID NO 41
/ LENGTH: 366
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: Incyte ID No: 7522915CD1
PCT-US03-25418-41

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Query Match          12.0%; Score 181; DB 1; Length 366;
Best Local Similarity 27.6%; Pred. No. 6.1e-07;
Matches 67; Conservative 23; Mismatches 65; Indels 88; Gaps 14;

QY 12 LVLVAVGSR---EHAYRGRVCAVRAHGDPRVSEFVQRVQPF-----LTTDGHRA 61
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 24 LHLALAGHTWYRYREBQDGRIC-----SSKXITTKYKPKCKSSGELTTCC----- 69
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 62 CSTYRTYRYAVYRSPGLAPARPRVYACCPGWRKTSG--LP---GACGAALICPPPCRNQGS 116
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 70 -----YRKK-----CCKGYKVLVGCICRBYDVAEAPCQGCCTDNRG 107
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 117 CVQPGRCRPAQWKRGT-----CQSDVDECGARRGG-CSPRCINTAGSYWCQWE 165
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 108 RV---LCTCYPGRYRREHRRKREKPYC-LDIDECASSNGTLCAHICINTLSSYCECRE 163
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 166 GHSLSADGTLVCPYKGGPRVAVPNTGVDAS-----MKBEVQLQSRV 207
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 164 GYRREDDKTKT--RQDK---YRVDITGHEKSENNWYKAGTCCATCKEFPYQMKQTVLQKQKI 219
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 208 DIL 210
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 220 ALL 222

RESULT 9
PCT-US03-25418-3
/ Sequence 3, Application PC/TUS0325418
/ GENERAL INFORMATION:
/ APPLICANT: INCYTE CORPORATION
/ APPLICANT: ELLIOTT VICKI S.
/ APPLICANT: KHARE, Reena
/ APPLICANT: EMERLING, Brooke M.
/ APPLICANT: KABLE, Amy E.
/ APPLICANT: TRAN, Uyen K.
/ APPLICANT: JIN, Pei
/ APPLICANT: BECHA, Shanva D.
/ APPLICANT: MARQUIS, Joseph P.
/ APPLICANT: SWARNAKAR, Anita
/ APPLICANT: CHAWLA, Nandinder K.
/ APPLICANT: RAMKUMAR, Jayalaxmi
/ APPLICANT: HAPALIA, Aaril J.A.
/ APPLICANT: LEB, Soo Yeun
/ APPLICANT: JIANG, Xin

```

```

/ APPLICANT: JACKSON, Alan A.
/ APPLICANT: RICHARDSON, Thomas W.
/ APPLICANT: BLAKE, Julie J.
/ APPLICANT: WANG, Jonathan T.
/ APPLICANT: CHIEN, David
/ APPLICANT: YANG, Yonphong G.
/ TITLE OF INVENTION: CELL ADHESION AND EXTRACELLULAR MATRIX PROTEINS
/ FILE REFERENCE: PR-1500 PCT
/ CURRENT APPLICATION NUMBER: PCT/US03/25418
/ CURRENT FILING DATE: 2003-08-12
/ PRIOR APPLICATION NUMBER: US 60/403,781
/ PRIOR FILING DATE: 2002-08-13
/ PRIOR APPLICATION NUMBER: US 60/407,034
/ PRIOR FILING DATE: 2002-08-30
/ PRIOR APPLICATION NUMBER: US 60/410,566
/ PRIOR FILING DATE: 2002-09-13
/ PRIOR APPLICATION NUMBER: US 60/413,482
/ PRIOR FILING DATE: 2002-09-24
/ PRIOR APPLICATION NUMBER: US 60/413,890
/ PRIOR FILING DATE: 2002-09-25
/ PRIOR APPLICATION NUMBER: US 60/424,904
/ PRIOR FILING DATE: 2002-11-08
/ PRIOR APPLICATION NUMBER: US 60/426,222
/ PRIOR FILING DATE: 2002-11-13
/ NUMBER OF SEQ ID NOS: 84
/ SOFTWARE: PERL Program
/ SEQ ID NO 3
/ LENGTH: 393
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: Incyte ID No: 7513607CD1
PCT-US03-25418-3

```

```

Query Match          11.7%; Score 176.5; DB 1; Length 393;
Best Local Similarity 27.4%; Pred. No. 1.5e-06;
Matches 55; Conservative 16; Mismatches 65; Indels 65; Gaps 8;

QY 54 TTCGHRKACSTYRTYRYAVYRSPGLAPAR--RAVCCGWRKTSGLPACGAALIC-QPPC 111
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 86 TPADGRKRKRSKYLVDHEVHTFCNPNRFLVGVSSVVCDFNGTWTGEPHCRGISSECSGQPC 145
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 112 RNGSGCVO-----PGR-----C 123
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 146 QNGFTCVGAVNQYRCICRPRGRTGNRCQHQAQTAPRBSGVAGDSAPRAQVBRACQC 205
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 124 RCPAGWR-----GPTCSVDVDECGARRGCPQ--RCINTAGSYWC---QCWEGHSLADG 173
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 206 SCEAGFHLISGAAGDSVQCQDVECVLQVPCQGTTCINTGSSFGCVSPECEPGE-----SG 260
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
QY 174 TLCVPGKGGPRVAVPNTGVDS 194
   ||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 261 NVSIVKTSVPCERNPCPMDS 281

RESULT 10
US-60-490-890-481
/ Sequence 481, Application US/60490890
/ GENERAL INFORMATION:
/ APPLICANT: Li, Martha
/ APPLICANT: Rupnow, Brent A.
/ APPLICANT: Webster, Kevin R.
/ APPLICANT: Jackson, Donald
/ APPLICANT: Wong, Tai W.
/ TITLE OF INVENTION: BIOMARKERS OF CYCLIN-DEPENDENT KINASE MODULATION
/ FILE REFERENCE: D0310 PSP
/ CURRENT APPLICATION NUMBER: US/60/490,890
/ CURRENT FILING DATE: 2003-07-29
/ NUMBER OF SEQ ID NOS: 2779
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 481
/ LENGTH: 2871

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TYPE: PRT
ORGANISM: Homo sapiens
US-60-490-890-481

Query Match 11.7%; Score 176.5; DB 7; Length 2871;
Best Local Similarity 22.7%; Pred. No. 1.4e-05;
Matches 59; Conservative 19; Mismatches 79; Indels 103; Gaps 8;

QY 26 PGRVCAVRAHGDPPVSESVFORVYQPLFTTCDGHR---ACSTYRTYRTAVYRSPGLADA 82
DB 75 PGNMCIYPIICHSQGDGFCR---PMMCTCPSGQIAPSCGS-RSQHONITCMNNGSGCS 130
QY 83 RPRVACCPGWRKRTSGLPGAICAICQPCRNNGSCVQPCRCRCPAAGWRTDTCQ----- 135
DB 131 DDHCCQKGYIGTHT-----CGQPVCESSGCLNGRCVAPRKACTYGTGTCQCEBDYRTGP 185
QY 136 -----S 136
DB 186 FTTVSNMCCGOLSGIVCTKTLCAATVGRAMGHPCEMCPAOPHPRCRGRFINIRTAQO 245
QY 137 DVDECSARRGGCP-QRCINTAGSYWCQCEGHSLSADGTLG-----VPRGG--- 181
DB 246 DVDECOALPGLCGGNCINTVSSFECKCPAGHKMLNVSQKCEDIDECSTIPGICRGGECT 305
QY 182 -----PBRVAPNPTG 191
DB 306 NTVSSYFCCKPRGPFYTSPPDG 325

RESULT 11

US-60-487-610-1941
Sequence 1941, Application US/60487610
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01469
CURRENT APPLICATION NUMBER: US/60/487, 610
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 97101
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 1941
LENGTH: 1587
TYPE: PRT
ORGANISM: Homo sapiens
US-60-487-610-1941

Query Match 11.7%; Score 176; DB 7; Length 1587;
Best Local Similarity 39.8%; Pred. No. 7.9e-06;
Matches 39; Conservative 6; Mismatches 41; Indels 12; Gaps 3;
QY 82 ARPRVACCPGWRKRTSGLPGAICAICQPCRNNGSCVQPCRCRCPAAGWRTDTCOSD 139
DB 625 AAPHGASQDQDVDECTQSPGLGCRGACKN-----LPGSFRVCVCPAGFRSACBEDVD 675
QY 140 EGSARRGGC-PQRCINTAGSYWCQCEGHSLSADGTLG 176
DB 676 ECAQEPPEPQGRCDNTAGSFFHCACPAFRSRGPAFC 713

RESULT 12

US-60-487-610-2570
Sequence 2570, Application US/60487610
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01469
CURRENT APPLICATION NUMBER: US/60/487, 610

CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 97101
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 2570
LENGTH: 2321
TYPE: PRT
ORGANISM: Homo sapiens
US-60-487-610-2570

Query Match 11.7%; Score 175.5; DB 7; Length 2321;
Best Local Similarity 34.5%; Pred. No. 1.3e-05;
Matches 50; Conservative 14; Mismatches 44; Indels 37; Gaps 11;
QY 56 CDGHRACSTYRTYRTAVYRSPGLAPARRVAC-CRQWKR--TSGLPGAICAICAICQPCRCR 112
DB 87 CAGREVCQS-----SVYAGTARFSCRCRPRFRGDDCSLPPPC-----LSSFCA 129
QY 113 NNGSG-VQP-GR-CRCPAAGWRTDTCQSDVDECC---SARRGGCPQRCINTAGSYWCQ 164
DB 130 HGARCQVGPDDGFLCSCPPGYQGRSCRSDVDDECRVGEPCRRHGG---TCLNTPGSPRCQCP 186
QY 165 EGHLSADGTLGCVPRKGPBRVAPNP 189
DB 187 AGYT-----GPLCENPVP-CAPSP 205

RESULT 13

US-60-485-450-1335
Sequence 1335, Application US/60485450
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: VIRUS-INFECTED SUBJECTS, METHODS OF DETECTION AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLO01470
CURRENT APPLICATION NUMBER: US/60/485, 450
CURRENT FILING DATE: 2003-07-09
NUMBER OF SEQ ID NOS: 47859
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 1335
LENGTH: 671
TYPE: PRT
ORGANISM: Homo sapiens
US-60-485-450-1335

Query Match 11.6%; Score 175; DB 7; Length 671;
Best Local Similarity 33.1%; Pred. No. 3.5e-06;
Matches 60; Conservative 10; Mismatches 57; Indels 54; Gaps 13;
QY 25 RPRRV-----CAVRHAGDPVSESVFORVYQPLFTTCDGHRACSTYRTYRTAVYRSPG 78
DB 307 RPFRLIDLDLVYTCASR---NPGSSS-----PCRGATCV----- 337
QY 79 LAPARRVAC-CP-GWKRKTSGLPGAICAICQPCRNNGSCVQ-PCRCRCPAAGWRTDTCOSD 130
DB 131 LPHKGNWYTKRCPPQGYQLDSSQGLDCVVDVDECDSDPCAQ--ECVNTPGGFRCECWNVGYRPG 395

QY 131 --GDTQSDVDECSARRGGCPQRCINTAGSYWCQCEGHSLSA-DGTL-----CVPRGG 181
DB 396 GPGEGACQDQDVDECALGRSPCAQCGTNTDGSFFHCSEBYVLAEGDTGQDQDVDECVGCG 455
QY 182 P 182
DB 456 P 456

RESULT 14

US-60-487-610-2260
Sequence 2260, Application US/60487610
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele

```

; APPLICANT: HUANG, Hongjin
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
; TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001469
; CURRENT APPLICATION NUMBER: US/60/487,610
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ. ID NOS: 97101
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ. ID NO 2260
; LENGTH: 1247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-487-610-2260

```

```

Query Match      11.5%; Score 173.5; DB 7; Length 1247;
Best Local Similarity 25.8%; Pred. No. 9.3e-06;
Matches 80; Conservative 23; Mismatches 98; Indels 109; Gaps 18;

```

```

QY 20 TEHAVRPRRV-----CAVRAHG-----DPVSESFVQRYVYQPFLLTGGDHRACSTYR 66
DB 681 TNACRPPRPTQTCTCCSIFRQDGRCTYDIDCSF-----QP--SVCGSHITGNH 730
QY 67 TIYRTAYRSPGLAPARPRYACCPGKRTSGLPACGAALCPP-----CRNG----- 114
DB 731 -----PGRFRCCEVGEYQFSD--EGTCVAAVDQRPINVCETGLHNCIDIPQR 774
QY 115 GSCVQVQ-----RCRCAGMRGD--TCQSDVDECSARGGCPORCTINTAGSYWCQWEGHS 168
DB 775 AQCITYGGSSYTCCLPGRFSGDQACQ--DVDECQPSRCHDAPFCYNTPPSFTQCCKRGY- 832
QY 169 ISADGTLVCP-----KGGPRVAVNPTG----- 191
DB 833 -GGDGRRCVGEVEKRCQHERHILGAAAGATPQRPPIRPGLFVPEBCDAHGYAPVQCHG 891
QY 192 -----VDSAMKEVQRLQSRVLDLEKQLVLAIRL-SLSQALEHGLPDPGSLVYS 243
DB 892 STGYCWCVDPRDGR-EVEGRTTRPGMTPPCLSTVAPPIHQRPVAVTAVIPLP-PGTHLL-- 947
QY 244 PQLGRIDSL 253
DB 948 FAQTGKIERYL 957

```

```

RESULT 15
PCT-US02-24483-4
; Sequence 4 Application PC/TUS0224483
; GENERAL INFORMATION:
; APPLICANT: Curagen Corp. et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-416A-061
; CURRENT APPLICATION NUMBER: PCT/US02/24483
; CURRENT FILING DATE: 2002-08-02
; PRIOR APPLICATION NUMBER: 60/309,501
; PRIOR FILING DATE: 2001-08-02
; PRIOR APPLICATION NUMBER: 60/323,994
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/373,814
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/310,291
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 60/310,951
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/310,544
; PRIOR FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: 60/311,292
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 60/311,979
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: 60/313,201
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: 60/312,892
; PRIOR FILING DATE: 2001-08-16

```

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; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ. ID NOS: 327
; SOFTWARE: CuraseqList version 0.1
; SEQ. ID NO 4
; LENGTH: 604
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-24483-4

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Query Match      11.2%; Score 168.5; DB 1; Length 604;
Best Local Similarity 24.1%; Pred. No. 9.8e-06;
Matches 60; Conservative 16; Mismatches 78; Indels 95; Gaps 9;

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QY 74 RSRPGLAPARR-----YACRPGKRTSGLPACGAALCPPCRNNGSCVQPG 121
DB 27 RRPFGHFAERRRRLGPHVCLSGFSGCCPQWAPSMWG-GGHCTLPLCSFRC-GSGICIAFN 84
QY 122 RCRCPAGMRGDTCC-----SPVD 139
DB 85 VCSQDQDGGGATCPETHGRCGERYGDLLTCSHGCOEVARVCGFSMTETAVGIRCTPID 144
QY 140 BCSARRGGCPORCTINTAGSYWCQWEGHSLAD-----GTLVCPK----- 179
DB 145 ECVT--SSCBEHCVMTEGGFVCECGPMQLSADRHSCQDTDECLGTPCQQRCKNSIGSYK 202
QY 180 -----GGPRVAVNPTGV--DSAMKEVQRLQSRVLDLEKQLVLAIRLPHLSLQ 227
DB 203 CSCRTGFHLHGRHRSVAFPRVAVLAPSAIILPQRHPSKMLLILPAGRPALSPGHSPPS- 261
QY 228 ALEHGLPDP 236
DB 262 ----GAPGP 266

```

```

Search completed: September 10, 2003, 17:23:33
Job time : 22 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 10, 2003, 17:13:08 ; Search time 404 Seconds.
(without alignments)
614.871 Million cell updates/sec

Title: US-09-978-191A-506

Perfect score: 1505

Sequence: 1 MRGSEVLLMVLVAVGT.....SEQISFLERQLGSCCKKDS 273

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 5728757 seqs, 909918778 residues 5728757

Total number of hits satisfying chosen parameters: 5728757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending_Patents_AA_Main:*
1: /cgn2_6/ptodata/1/paa/PCRTUS_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US06_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_COMB.pep:*
5: /cgn2_6/ptodata/1/paa/US081_COMB.pep:*
6: /cgn2_6/ptodata/1/paa/US082_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US083_COMB.pep:*
8: /cgn2_6/ptodata/1/paa/US084_COMB.pep:*
9: /cgn2_6/ptodata/1/paa/US085_COMB.pep:*
10: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*
11: /cgn2_6/ptodata/1/paa/US087_COMB.pep:*
12: /cgn2_6/ptodata/1/paa/US088_COMB.pep:*
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16: /cgn2_6/ptodata/1/paa/US092_COMB.pep:*
17: /cgn2_6/ptodata/1/paa/US093_COMB.pep:*
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29: /cgn2_6/ptodata/1/paa/US103_COMB.pep:*
30: /cgn2_6/ptodata/1/paa/US104_COMB.pep:*
31: /cgn2_6/ptodata/1/paa/US106_COMB.pep:*
32: /cgn2_6/ptodata/1/paa/US60_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1505	100.0	273	1	PCT-US99-08900-2 Sequence 2, Appl1

Query Match	Score	DB 1	Length	Best Local Similarity	Pred. No.	Indels	Gaps
Matches 273;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;			

ALIGNMENTS

RESULT 1
PCT-US99-08900-2
Sequence 2, Application PC/TUS9908900
GENERAL INFORMATION:
APPLICANT: Millennium Biotherapeutics, Inc.
TITLE OF INVENTION: NOVEL MOLECULES OF THE T125-RELATED PROTEIN FAMILY
FILE REFERENCE: 09404/074W01
CURRENT FILING DATE: 1999-04-23
EARLIER FILING DATE: 1998-04-24
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSeq for Windows Version 3.0
ORGANISM: Homo sapiens
PCT-US99-08900-2

QY 1 MRGSOEVLMLLVLAVGTEHAYRPPGRVCAVARAHGDPVSESFVORVYQPFLLTCCDGR 60
 Db 1 MRGSOEVLMLLVLAVGTEHAYRPPGRVCAVARAHGDPVSESFVORVYQPFLLTCCDGR 60
 QY 61 ACSTYRTTYRTAYRRSPGLAPARPRYACCPGMRKRTSGLPGACGAIICOPPCRNNGSSCVQP 120
 Db 61 ACSTYRTTYRTAYRRSPGLAPARPRYACCPGMRKRTSGLPGACGAIICOPPCRNNGSSCVQP 120
 QY 121 GRRCPCAGMRGDTCCSDVDECSARRGGCPORCINTAGSYWCQCWEGHSLSDGTLCPVKG 180
 Db 121 GRRCPCAGMRGDTCCSDVDECSARRGGCPORCINTAGSYWCQCWEGHSLSDGTLCPVKG 180
 QY 181 GPPRVAHPNPTGVDSAMKEEVORLQSRVDLLEKQLVLAAPLHSLASQALEHGLPDPGSL 240
 Db 181 GPPRVAHPNPTGVDSAMKEEVORLQSRVDLLEKQLVLAAPLHSLASQALEHGLPDPGSL 240
 QY 241 VHSFOQLGRIDSLSEQISFLBEOIGSSCSCKKDS 273
 Db 241 VHSFOQLGRIDSLSEQISFLBEOIGSSCSCKKDS 273

RESULT 2
 US-09-065-363-2
 ; Sequence 2, Application US/09065363
 ; GENERAL INFORMATION:
 ; APPLICANT: Holtzman, Douglas
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE
 ; NUMBER OF SEQUENCES: 4
 ; CORRESPONDENCE ADDRESSES:
 ; * ADDRESSEE: Fish & Richardson P.C.
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; OPERATING SYSTEM: Windows95
 ; SOFTWARE: FASTSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/065,363
 ; FILING DATE: 23-APR-1998
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Meiklejohn, Ph.D., Anita L.
 ; REGISTRATION NUMBER: 35,283
 ; REFERENCE/DOCKET NUMBER: 09404/048001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617/542-5070
 ; TELEFAX: 617/542-8906
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 273 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FRAGMENT TYPE: internal
 ; US-09-065-363-2

Query Match 100.0%; Score 1505; DB 14; Length 273;
 Best Local Similarity 100.0%; Pred. No. 4.6e-113;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSOEVLMLLVLAVGTEHAYRPPGRVCAVARAHGDPVSESFVORVYQPFLLTCCDGR 60
 Db 1 MRGSOEVLMLLVLAVGTEHAYRPPGRVCAVARAHGDPVSESFVORVYQPFLLTCCDGR 60
 QY 61 ACSTYRTTYRTAYRRSPGLAPARPRYACCPGMRKRTSGLPGACGAIICOPPCRNNGSSCVQP 120
 Db 61 ACSTYRTTYRTAYRRSPGLAPARPRYACCPGMRKRTSGLPGACGAIICOPPCRNNGSSCVQP 120
 QY 121 GRRCPCAGMRGDTCCSDVDECSARRGGCPORCINTAGSYWCQCWEGHSLSDGTLCPVKG 180
 Db 121 GRRCPCAGMRGDTCCSDVDECSARRGGCPORCINTAGSYWCQCWEGHSLSDGTLCPVKG 180

Db 61 ACSTYRTTYRTAYRRSPGLAPARPRYACCPGMRKRTSGLPGACGAIICOPPCRNNGSSCVQP 120
 QY 121 GRRCPCAGMRGDTCCSDVDECSARRGGCPORCINTAGSYWCQCWEGHSLSDGTLCPVKG 180
 Db 121 GRRCPCAGMRGDTCCSDVDECSARRGGCPORCINTAGSYWCQCWEGHSLSDGTLCPVKG 180
 QY 181 GPPRVAHPNPTGVDSAMKEEVORLQSRVDLLEKQLVLAAPLHSLASQALEHGLPDPGSL 240
 Db 181 GPPRVAHPNPTGVDSAMKEEVORLQSRVDLLEKQLVLAAPLHSLASQALEHGLPDPGSL 240
 QY 241 VHSFOQLGRIDSLSEQISFLBEOIGSSCSCKKDS 273
 Db 241 VHSFOQLGRIDSLSEQISFLBEOIGSSCSCKKDS 273

RESULT 3
 US-09-065-363A-2
 ; Sequence 2, Application US/09065363A
 ; GENERAL INFORMATION:
 ; APPLICANT: Holtzman, Douglas
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE T125-RELATED
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESSES:
 ; ADDRESSER: Fish & Richardson P.C.
 ; STREET: 225 Franklin Street
 ; CITY: Boston
 ; STATE: MA
 ; COUNTRY: USA
 ; ZIP: 02110-2804
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; OPERATING SYSTEM: Windows95
 ; SOFTWARE: FASTSEQ for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/065,363A
 ; FILING DATE: 23-APR-1998
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Meiklejohn, Ph.D., Anita L.
 ; REGISTRATION NUMBER: 35,283
 ; REFERENCE/DOCKET NUMBER: 09404/048001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617/542-5070
 ; TELEFAX: 617/542-8906
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 273 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FRAGMENT TYPE: internal
 ; US-09-065-363A-2

Query Match 100.0%; Score 1505; DB 14; Length 273;
 Best Local Similarity 100.0%; Pred. No. 4.6e-113;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSOEVLMLLVLAVGTEHAYRPPGRVCAVARAHGDPVSESFVORVYQPFLLTCCDGR 60
 Db 1 MRGSOEVLMLLVLAVGTEHAYRPPGRVCAVARAHGDPVSESFVORVYQPFLLTCCDGR 60
 QY 61 ACSTYRTTYRTAYRRSPGLAPARPRYACCPGMRKRTSGLPGACGAIICOPPCRNNGSSCVQP 120
 Db 61 ACSTYRTTYRTAYRRSPGLAPARPRYACCPGMRKRTSGLPGACGAIICOPPCRNNGSSCVQP 120
 QY 121 GRRCPCAGMRGDTCCSDVDECSARRGGCPORCINTAGSYWCQCWEGHSLSDGTLCPVKG 180
 Db 121 GRRCPCAGMRGDTCCSDVDECSARRGGCPORCINTAGSYWCQCWEGHSLSDGTLCPVKG 180

Db 121 GRCRCPAGWRGDTCCSDVDECSARRGCGPCRCINTAGSYWCOCWEGHSLISADGTLCPVPGK 180
 Qy 181 GPPRVA PNTGVD SAMKEVORLQSRVLDLLEKQLQVLAPLPHSLASQALEHGLPDPGSLI 240
 Db 181 GPPRVA PNTGVD SAMKEVORLQSRVLDLLEKQLQVLAPLPHSLASQALEHGLPDPGSLI 240
 Qy 241 VHSFOOLGRIDSLSEGISFLEBQLGSCCKKDS 273
 Db 241 VHSFOOLGRIDSLSEGISFLEBQLGSCCKKDS 273

RESULT 4
 US-09-298-531-2
 ; Sequence 2, Application US/09298531
 ; GENERAL INFORMATION:
 ; APPLICANT: Holtzman, Douglas A.
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE T125-RELATED PROTEIN FAMILY
 ; FILE REFERENCE: 09404/074001
 ; CURRENT APPLICATION NUMBER: US/09/298,531
 ; EARLIER FILING DATE: 1999-04-23
 ; EARLIER APPLICATION NUMBER: US 09/065,363
 ; NUMBER OF SEQ ID NOS: 23
 ; SOFTWARE: FaastSeq for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 273
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-298-531-2

Query Match 100.0%; Score 1505; DB 16; Length 273;
 Best Local Similarity 100.0%; Pred. No. 4,66-113;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGSEVILMLLVLA VGTETAYRPPRRVCAVRAHGDVSSFPVQRYVQPELTTCDGHR 60
 Db 1 MRGSEVILMLLVLA VGTETAYRPPRRVCAVRAHGDVSSFPVQRYVQPELTTCDGHR 60
 Qy 61 ACSTRTTYRTYRTRSSPGIAPRPRVYACCPGKRTSGLPAGAGAIICPPCGNCGSCVQP 120
 Db 61 ACSTRTTYRTYRTRSSPGIAPRPRVYACCPGKRTSGLPAGAGAIICPPCGNCGSCVQP 120
 Qy 121 GRCRCPAGWRGDTCCSDVDECSARRGCGPCRCINTAGSYWCOCWEGHSLISADGTLCPVPGK 180
 Db 121 GRCRCPAGWRGDTCCSDVDECSARRGCGPCRCINTAGSYWCOCWEGHSLISADGTLCPVPGK 180
 Qy 181 GPPRVA PNTGVD SAMKEVORLQSRVLDLLEKQLQVLAPLPHSLASQALEHGLPDPGSLI 240
 Db 181 GPPRVA PNTGVD SAMKEVORLQSRVLDLLEKQLQVLAPLPHSLASQALEHGLPDPGSLI 240
 Qy 241 VHSFOOLGRIDSLSEGISFLEBQLGSCCKKDS 273
 Db 241 VHSFOOLGRIDSLSEGISFLEBQLGSCCKKDS 273

RESULT 5
 US-09-380-138-506
 ; Sequence 506, Application US/09380138
 ; GENERAL INFORMATION:
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Gurney, Austin
 ; APPLICANT: Yuan, Jean
 ; APPLICANT: Baker, Kevin P.
 ; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding the Same
 ; FILE REFERENCE: P2630R1E
 ; CURRENT APPLICATION NUMBER: US/09/380,138
 ; CURRENT FILING DATE: 1999-08-25
 ; PRIOR APPLICATION NUMBER: PCT/US99/05028
 ; PRIOR FILING DATE: 1999-03-08
 ; PRIOR APPLICATION NUMBER: US 60/077,450
 ; PRIOR FILING DATE: 1998-03-10

;; PRIOR APPLICATION NUMBER: US 60/077,632
 ;; PRIOR FILING DATE: 1998-03-11
 ;; PRIOR APPLICATION NUMBER: US 60/077,641
 ;; PRIOR FILING DATE: 1998-03-11
 ;; PRIOR APPLICATION NUMBER: US 60/077,649
 ;; PRIOR FILING DATE: 1998-03-11
 ;; PRIOR APPLICATION NUMBER: US 60/077,791
 ;; PRIOR FILING DATE: 1998-03-12
 ;; PRIOR APPLICATION NUMBER: US 60/078,004
 ;; PRIOR FILING DATE: 1998-03-13
 ;; PRIOR APPLICATION NUMBER: US 09/040,220
 ;; PRIOR FILING DATE: 1998-03-17
 ;; PRIOR APPLICATION NUMBER: US 60/078,886
 ;; PRIOR FILING DATE: 1998-03-20
 ;; PRIOR APPLICATION NUMBER: US 60/078,910
 ;; PRIOR FILING DATE: 1998-03-20
 ;; PRIOR APPLICATION NUMBER: US 60/078,939
 ;; PRIOR FILING DATE: 1998-03-20
 ;; PRIOR APPLICATION NUMBER: US 60/078,936
 ;; PRIOR FILING DATE: 1998-03-20
 ;; PRIOR APPLICATION NUMBER: US 60/079,294
 ;; PRIOR FILING DATE: 1998-03-25
 ;; PRIOR APPLICATION NUMBER: US 60/079,556
 ;; PRIOR FILING DATE: 1998-03-26
 ;; PRIOR APPLICATION NUMBER: US 60/079,728
 ;; PRIOR FILING DATE: 1998-03-27
 ;; PRIOR APPLICATION NUMBER: US 60/079,786
 ;; PRIOR FILING DATE: 1998-03-27
 ;; PRIOR APPLICATION NUMBER: US 60/079,664
 ;; PRIOR FILING DATE: 1998-03-27
 ;; PRIOR APPLICATION NUMBER: US 60/079,689
 ;; PRIOR FILING DATE: 1998-03-27
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 ;; PRIOR FILING DATE: 1998-03-31
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 ;; PRIOR FILING DATE: 1998-04-15
 ;; PRIOR APPLICATION NUMBER: US 60/081,817

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PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: US 60/082,569
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PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: US 60/082,804
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: US 60/082,704
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: US 60/082,767
PRIOR FILING DATE: 1998-04-23
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PRIOR FILING DATE: 1998-04-23
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PRIOR FILING DATE: 1998-04-29
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PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: US 60/083,742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: US 60/084,366
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: US 60/084,441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: US 60/084,414
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: US 60/084,640
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: US 60/084,639
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: US 60/084,637
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: US 60/084,643
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: US 60/084,598
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: US 60/084,600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: US 60/084,627
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: US 60/085,339
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: US 60/085,338
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: US 60/085,323
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: US 60/085,573
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: US 60/085,697
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: US 60/085,580
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: US 60/085,579
PRIOR FILING DATE: 1998-05-15

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PRIOR APPLICATION NUMBER: US 60/085,704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: US 60/085,582
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: US 60/085,689
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: US 60/085,700
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: US 60/086,023
PRIOR FILING DATE: 1998-05-18
PRIOR APPLICATION NUMBER: US 60/086,486
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: US 60/086,414
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: US 60/086,392
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: US 60/086,430
PRIOR FILING DATE: 1998-05-22
PRIOR APPLICATION NUMBER: US 60/087,208
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: US 60/087,098
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: US 60/087,106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: US 60/094,651
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: US 60/100,038
PRIOR FILING DATE: 1998-09-11
NUMBER OF SEQ ID NOS: 538
SEQ ID NO 506
LENGTH: 273
TYPE: PRT
ORGANISM: Homo sapiens
US-09-380-138-506

Query Match 100.0%; Score 1505; DB 17; Length 273;
Best Local Similarity 100.0%; Pred. No. 4.6e-113;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSEVLLMVLIVAVGTEHAYRPRRVCANVAHGPVSEFVQRYVYQPLTTCCGHR 60
DB 1 MRGSEVLLMVLIVAVGTEHAYRPRRVCANVAHGPVSEFVQRYVYQPLTTCCDHR 60
QY 61 ACSTRTTYRTAYRSPPLAPRPPYACCPGKRTSGLPAGCAAIQPPCRNGSSCVQP 120
DB 61 ACSTRTTYRTAYRSPPLAPRPPYACCPGKRTSGLPAGCAAIQPPCRNGSSCVQP 120
QY 121 GRCRCPPAGMRDPTCQSDVDECSARRGGCPQRCINTAGSYWCQWEGHSLSDGTLVCPKG 180
DB 121 GRCRCPPAGMRDPTCQSDVDECSARRGGCPQRCINTAGSYWCQWEGHSLSDGTLVCPKG 180
QY 181 GPRPVAAPPTVSDSMKKEVQRLQSRVDLLEKQLVLIAPLHSLASQALEHGLPDPGSL 240
DB 181 GPRPVAAPPTVSDSMKKEVQRLQSRVDLLEKQLVLIAPLHSLASQALEHGLPDPGSL 240
QY 241 VHSFOQLGRIDLSLEQISFLBEQIGSCSCKKDS 273
DB 241 VHSFOQLGRIDLSLEQISFLBEQIGSCSCKKDS 273

RESULT 6
US-09-380-138-508
Sequence 508, Application US/09380138
GENERAL INFORMATION:
APPLICANT: Wood, William I.
APPLICANT: Goddard, Audrey
APPLICANT: Gurney, Austin
APPLICANT: Yuan, Jean
APPLICANT: Baker, Kevin P.
TITLE OF INVENTION: Novel polypeptides and Nucleic Acids Encoding the Same
FILE REFERENCE: P2630RIE
CURRENT APPLICATION NUMBER: US/09/380,138
CURRENT FILING DATE: 1999-08-25

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PRIORITY APPLICATION NUMBER: US 60/085,580
PRIORITY FILING DATE: 1998-05-15
PRIORITY APPLICATION NUMBER: US 60/085,579
PRIORITY FILING DATE: 1998-05-15
PRIORITY APPLICATION NUMBER: US 60/085,704
PRIORITY FILING DATE: 1998-05-15
PRIORITY APPLICATION NUMBER: US 60/085,582
PRIORITY FILING DATE: 1998-05-15
PRIORITY APPLICATION NUMBER: US 60/085,689
PRIORITY FILING DATE: 1998-05-15
PRIORITY APPLICATION NUMBER: US 60/085,700
PRIORITY FILING DATE: 1998-05-15
PRIORITY APPLICATION NUMBER: US 60/086,023
PRIORITY FILING DATE: 1998-05-18
PRIORITY APPLICATION NUMBER: US 60/086,486
PRIORITY FILING DATE: 1998-05-22
PRIORITY APPLICATION NUMBER: US 60/086,414
PRIORITY FILING DATE: 1998-05-22
PRIORITY APPLICATION NUMBER: US 60/086,392
PRIORITY FILING DATE: 1998-05-22
PRIORITY APPLICATION NUMBER: US 60/086,430
PRIORITY FILING DATE: 1998-05-22
PRIORITY APPLICATION NUMBER: US 60/087,208
PRIORITY FILING DATE: 1998-05-28
PRIORITY APPLICATION NUMBER: US 60/087,098
PRIORITY FILING DATE: 1998-05-28
PRIORITY APPLICATION NUMBER: US 60/087,106
PRIORITY FILING DATE: 1998-05-28
PRIORITY APPLICATION NUMBER: US 60/094,651
PRIORITY FILING DATE: 1998-07-30
PRIORITY APPLICATION NUMBER: US 60/100,038
PRIORITY FILING DATE: 1998-09-11
NUMBER OF SEQ ID NOS: 538
SEQ ID NO: 508
LENGTH: 273
TYPE: PRT
ORGANISM: Homo sapiens
US-09-380-138-508

```

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Query Match      100.0%; Score 1505; DB 17; Length 273;
Best Local Similarity 100.0%; Pred. No. 4,6e-113;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRSQEVLLMMLLVLA VAGSTEHAYRPPGRVCAVRAHAGDPVSESFVQRYOYOPFLITTCDDHR 60
DB 1 MRSQEVLLMMLLVLA VAGSTEHAYRPPGRVCAVRAHAGDPVSESFVQRYOYOPFLITTCDDHR 60
OY 61 ACSTYRTTYRTRAYRSRPGIAPARPRVYACCPGWKRTSGLPAGCGAAICOPPCRNNGSSCVQP 120
DB 61 ACSTYRTTYRTRAYRSRPGIAPARPRVYACCPGWKRTSGLPAGCGAAICOPPCRNNGSSCVQP 120
OY 121 GRCRCFAGMRGDTCCSDVDECSARRGCGPQRCINTAGSYWCQCBGHSLSADGTLCPVPG 180
DB 121 GRCRCFAGMRGDTCCSDVDECSARRGCGPQRCINTAGSYWCQCBGHSLSADGTLCPVPG 180
OY 181 GPPRVAHPNPTGVDSAMKEEVORLQSRVDLLEKQLQVLAPLHSLASQALEHGLPDPGSL 240
DB 181 GPPRVAHPNPTGVDSAMKEEVORLQSRVDLLEKQLQVLAPLHSLASQALEHGLPDPGSL 240
OY 241 VHSFOQLGRIDSLSEQISFLBEQLGSCSCCKKDS 273
DB 241 VHSFOQLGRIDSLSEQISFLBEQLGSCSCCKKDS 273

RESULT 7
US-09-790-264-10
Sequence 10, Application US/09790264
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas A.
APPLICANT: Goodheart, Andrew D.J.
APPLICANT: McCarthy, Sean A.
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
PROGNASTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER

```

```

TITLE OF INVENTION: USES
FILE REFERENCE: 07334-322001
CURRENT FILING DATE: 2001-02-21
PRIORITY APPLICATION NUMBER: US 09/065,661
PRIORITY FILING DATE: 1998-04-23
PRIORITY APPLICATION NUMBER: US 09/298,531
PRIORITY FILING DATE: 1999-04-23
PRIORITY APPLICATION NUMBER: US 09/065,363
PRIORITY FILING DATE: 1998-04-23
PRIORITY APPLICATION NUMBER: US 09/337,930
PRIORITY FILING DATE: 1999-06-22
PRIORITY APPLICATION NUMBER: US 09/102,705
PRIORITY FILING DATE: 1998-06-22
PRIORITY APPLICATION NUMBER: US 09/363,630
PRIORITY FILING DATE: 1999-07-29
PRIORITY APPLICATION NUMBER: US 09/124,538
PRIORITY FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 68
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 10
LENGTH: 273
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(22)
US-09-790-264-10

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Query Match      100.0%; Score 1505; DB 22; Length 273;
Best Local Similarity 100.0%; Pred. No. 4,6e-113;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRSQEVLLMMLLVLA VAGSTEHAYRPPGRVCAVRAHAGDPVSESFVQRYOYOPFLITTCDDHR 60
DB 1 MRSQEVLLMMLLVLA VAGSTEHAYRPPGRVCAVRAHAGDPVSESFVQRYOYOPFLITTCDDHR 60
OY 61 ACSTYRTTYRTRAYRSRPGIAPARPRVYACCPGWKRTSGLPAGCGAAICOPPCRNNGSSCVQP 120
DB 61 ACSTYRTTYRTRAYRSRPGIAPARPRVYACCPGWKRTSGLPAGCGAAICOPPCRNNGSSCVQP 120
OY 121 GRCRCFAGMRGDTCCSDVDECSARRGCGPQRCINTAGSYWCQCBGHSLSADGTLCPVPG 180
DB 121 GRCRCFAGMRGDTCCSDVDECSARRGCGPQRCINTAGSYWCQCBGHSLSADGTLCPVPG 180
OY 181 GPPRVAHPNPTGVDSAMKEEVORLQSRVDLLEKQLQVLAPLHSLASQALEHGLPDPGSL 240
DB 181 GPPRVAHPNPTGVDSAMKEEVORLQSRVDLLEKQLQVLAPLHSLASQALEHGLPDPGSL 240
OY 241 VHSFOQLGRIDSLSEQISFLBEQLGSCSCCKKDS 273
DB 241 VHSFOQLGRIDSLSEQISFLBEQLGSCSCCKKDS 273

RESULT 8
US-09-918-585A-506
Sequence 506, Application US/09918585A
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Bolstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.

```

APPLICANT: Hillan, Kenneth J
APPLICANT: Klavin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: Acids Encoding the Same
CURRENT APPLICATION NUMBER: US/09/918,585A
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/077450
PRIOR FILING DATE: 1998-03-10
PRIOR APPLICATION NUMBER: 60/077632
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077641
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
PRIOR APPLICATION NUMBER: 60/078886
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/078936
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PRIOR FILING DATE: 1998-03-27
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PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080107
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
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PRIOR FILING DATE: 1998-03-31
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PRIOR APPLICATION NUMBER: 60/082797
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/082796
PRIOR FILING DATE: 1998-04-23
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PRIOR FILING DATE: 1998-04-27
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083392
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PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/083742
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/084366
PRIOR FILING DATE: 1998-05-05
PRIOR APPLICATION NUMBER: 60/084414
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/084637

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/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084639
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084640
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084598
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084600
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084627
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/084643
/ PRIOR FILING DATE: 1998-05-07
/ PRIOR APPLICATION NUMBER: 60/085339
/ PRIOR FILING DATE: 1998-05-13
/ PRIOR APPLICATION NUMBER: 60/085338
/ PRIOR FILING DATE: 1998-05-13
/ PRIOR APPLICATION NUMBER: 60/085323
/ PRIOR FILING DATE: 1998-05-13
/ PRIOR APPLICATION NUMBER: 60/085582
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085700
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085689
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/ PRIOR FILING DATE: 1998-05-15
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/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085573
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085704
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085697
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/086023
/ PRIOR FILING DATE: 1998-05-18

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Query Match 100.0%; Score 1505; DB 24; Length 273;
Best Local Similarity 100.0%; Pred. No. 4,6e-113;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MRSQSEVLLMLLVLA VGGTEHAYRPPGRRVCAVRAHGDVSSFPVQRYVQPLTTCDDGR 60
DB 1 MRSQSEVLLMLLVLA VGGTEHAYRPPGRRVCAVRAHGDVSSFPVQRYVQPLTTCDDGR 60
QY 61 ACSYRRTYRTAYRBSRGLAPARPRYACCPGWRKRTSGLPGACGAACOPPCRNKGGSCVQP 120
DB 61 ACSYRRTYRTAYRBSRGLAPARPRYACCPGWRKRTSGLPGACGAACOPPCRNKGGSCVQP 120
QY 121 GRCRCFAGWRGDTCCSDVDECSARRRGGCFCPCINTAGSYWCOCWEGHSLSADGTLCPVPG 180
DB 121 GRCRCFAGWRGDTCCSDVDECSARRRGGCFCPCINTAGSYWCOCWEGHSLSADGTLCPVPG 180
QY 181 GPPRAVNPRTGVDSAMKEEVORIQSRVLLIEKQLQVLAPLHLSQALEHGLPDPGSL 240
DB 181 GPPRAVNPRTGVDSAMKEEVORIQSRVLLIEKQLQVLAPLHLSQALEHGLPDPGSL 240
QY 241 VHSFOOLGRIDSLSRQISFLEROLGSCGCKKDS 273
DB 241 VHSFOOLGRIDSLSRQISFLEROLGSCGCKKDS 273
RESULT 9
US-09-918-585A-508
; Sequence 508, Application US/09918585A
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Demoyers, Luc
; APPLICANT: Baton, Dan
; APPLICANT: Ferrara, Napoleone

```

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/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Fong, Sherman
/ APPLICANT: Gao, Wei-Qiang
/ APPLICANT: Gerber, Hanspeter
/ APPLICANT: Gerritsen, Mary E.
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Hillan, Kenneth J.
/ APPLICANT: Kljavin, Ivar J.
/ APPLICANT: Kuo, Sophia S.
/ APPLICANT: Napier, Mary A.
/ APPLICANT: Pan, James.
/ APPLICANT: Paoni, Nicholas F.
/ APPLICANT: Roy, Margaret Ann
/ APPLICANT: Shelton, David L.
/ APPLICANT: Stewart, Timothy A.
/ APPLICANT: Tumas, Daniel
/ APPLICANT: Williams, P. Mickey
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: Secured and Transmembrane Polypeptides and Nucleic
/ FILE REFERENCE: P2630P1C1
/ CURRENT APPLICATION NUMBER: US/09/918,585A
/ CURRENT FILING DATE: 2001-07-30
/ PRIOR APPLICATION NUMBER: 60/062250
/ PRIOR FILING DATE: 1997-10-17
/ PRIOR APPLICATION NUMBER: 60/064249
/ PRIOR FILING DATE: 1997-11-03
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/ PRIOR APPLICATION NUMBER: 60/066364
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/ PRIOR APPLICATION NUMBER: 60/079923
/ PRIOR FILING DATE: 1998-03-30
/ PRIOR APPLICATION NUMBER: 60/080105

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 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/080328
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 PRIOR APPLICATION NUMBER: 60/080334
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 PRIOR FILING DATE: 1998-05-15
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 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/086023
 PRIOR FILING DATE: 1998-05-18

Query Match 100.0%; Score 1505; DB 24; Length 273;
 Best Local Similarity 100.0%; Pred. No. 4.6e-113;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSEVLLMVLVAVGCTEHAIRPGRVCAVRAHGDVSESFVQRYVQPLTTCDGHR 60
 Db 1 MRGSEVLLMVLVAVGCTEHAIRPGRVCAVRAHGDVSESFVQRYVQPLTTCDGHR 60
 QY 61 AOSTYRTTYRTAVYRSPGLAARPRVYACCPGMRKRTSGIPGACGAATCCPPRRNGSSCVOP 120
 Db 61 AOSTYRTTYRTAVYRSPGLAARPRVYACCPGMRKRTSGIPGACGAATCCPPRRNGSSCVOP 120
 QY 121 GRRCPCPAGWRDTCOSVDVDECSARRGCCPQRCTINTAGSYWCQCMEGHLSADGTLCVPKG 180
 Db 121 GRRCPCPAGWRDTCOSVDVDECSARRGCCPQRCTINTAGSYWCQCMEGHLSADGTLCVPKG 180
 QY 181 GPPRVAENPPTGVDSAMKEEVORLOSRYVDLBEKQLVLAIPHLSIASQALBEHGLDPPGSL 240
 Db 181 GPPRVAENPPTGVDSAMKEEVORLOSRYVDLBEKQLVLAIPHLSIASQALBEHGLDPPGSL 240
 QY 241 VHSFQQLGRIRISLSEOTSFLEBOLGSCSCCKKDS 273
 Db 241 VHSFQQLGRIRISLSEOTSFLEBOLGSCSCCKKDS 273

RESULT 10

US-09-978-187B-506
 ; Sequence 506 Application US/09978187B
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrata, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
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 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
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 ; APPLICANT: Napier, Mary A.
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 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2630P1C5
 ; CURRENT APPLICATION NUMBER: US/09/978,187B
 ; CURRENT FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: 09/918585
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 ? PRIOR FILING DATE: 1998-05-15

Query Match 100.0%; Score 1505; DB 25; Length 273;
 Best Local Similarity 100.0%; Pred. No. 4,6e-113;

Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSEVLLMVLVAVGSTEHAHYRGRVCAVRAHGPVSESFVQRYVQPLTTCDDGHR 60
 DB 1 MRGSEVLLMVLVAVGSTEHAHYRGRVCAVRAHGPVSESFVQRYVQPLTTCDDGHR 60
 QY 61 ACSTYRTTYRTRRYSRPGLAAPARPRYACCPGKRTSGLPAGCAAIICPPCRNGSSCVQP 120
 DB 61 ACSTYRTTYRTRRYSRPGLAAPARPRYACCPGKRTSGLPAGCAAIICPPCRNGSSCVQP 120
 QY 121 GRRCRCPAGMRGDTCCSDVDECSARRGGCPORCINTNAGSYWCCGWSHLSIANDGTLCVKKG 180
 DB 121 GRRCRCPAGMRGDTCCSDVDECSARRGGCPORCINTNAGSYWCCGWSHLSIANDGTLCVKKG 180
 QY 181 GPPRVAVNPPTGVDSAMKEVQRLOQRVLDLBEKQLDLVLAFLHSLASQALEHGLPDPGSL 240
 DB 181 GPPRVAVNPPTGVDSAMKEVQRLOQRVLDLBEKQLDLVLAFLHSLASQALEHGLPDPGSL 240

DB 181 GPPRVAVNPPTGVDSAMKEVQRLOQRVLDLBEKQLDLVLAFLHSLASQALEHGLPDPGSL 240
 QY 241 VHSFOOLGRIDSLSRQISFLEBOLGSCCKKDS 273
 DB 241 VHSFOOLGRIDSLSRQISFLEBOLGSCCKKDS 273

RESULT 11
US-09-978-187B-508

? Sequence 508, Application US/09978187B
 ? GENERAL INFORMATION:
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 ? TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ? FILE REFERENCE: P2630PIC5
 ? CURRENT FILING DATE: 2001-10-15
 ? PRIOR APPLICATION NUMBER: US/09/978,187B
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Query Match 100.0%; Score 1505; DB 25; Length 273;
 Best Local Similarity 100.0%; Pred. No. 4,6e-113;
 Matches 273; Conservatve 0; Mismatches 0; Indels 0; Gaps 0;

CQ 1 MRGSOEVLMMWLVAVGTEHAYRPGRRVCVRAHDDPVSESPVORVYVOPFLTCCGHR 60
 Db 1 MRGSOEVLMMWLVAVGTEHAYRPGRRVCVRAHDDPVSESPVORVYVOPFLTCCGHR 60

QY 61 ACSTYRTYTRAVRSPBGLAPARPRYACCPBWKRTSGLPDAGCAIICPPPCRNSSCVOP 120
 Db 61 ACSTYRTYTRAVRSPBGLAPARPRYACCPBWKRTSGLPDAGCAIICPPPCRNSSCVOP 120
 QY 121 GRCRCAGWRGDTCCOSDVBCSARRGGCCPQRCNTNTGSGWCCOMBEHSLSAAGTLCVPRG 180
 Db 121 GRCRCAGWRGDTCCOSDVBCSARRGGCCPQRCNTNTGSGWCCOMBEHSLSAAGTLCVPRG 180
 QY 181 GPPRVAPNPTGVDSANKEEVORLQSRVDDLLEKQLQVLAPLHSLASQALEHGLPDPGSL 240
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 QY 241 VHSFOQLGRIDSLSEQISFLBEOIGSCKKDS 273
 Db 241 VHSFOQLGRIDSLSEQISFLBEOIGSCKKDS 273

RESULT 12

US-09-978-188A-506
 / Sequence 506, Application US/09978188A

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker Kevin P.
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 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2630P1C8
 CURRENT APPLICATION NUMBER: US/09/978,188A
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 PRIOR FILING DATE: 1998-04-21
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 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082804

PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082700
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082797
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082796
 PRIOR FILING DATE: 1998-04-23
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 PRIOR APPLICATION NUMBER: 60/083392
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 PRIOR APPLICATION NUMBER: 60/085573
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697
 PRIOR FILING DATE: 1998-05-15

Query Match 100.0%; Score 1505; DB 25; Length 273;
 Best Local Similarity 100.0%; Pred. No. 4.6e-113;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRGSEVLLMVLVIAVNGSTEARPRGRVCAVNAHGPVSESVRYORVYOPFLITTCGHR 60
 Db 1 MRGSEVLLMVLVIAVNGSTEARPRGRVCAVNAHGPVSESVRYORVYOPFLITTCGHR 60
 Qy 61 ACSTYRTTYRTAYRRSPGLAIPARPRYACCPGPKRTSGIPGACGAALICQPPCRNNGSCTQP 120
 Db 61 ACSTYRTTYRTAYRRSPGLAIPARPRYACCPGPKRTSGIPGACGAALICQPPCRNNGSCTQP 120
 Qy 121 GRCRCPAGWRGDTCCSDVDECSARRGGCPQRCINTAGSYWCQCWEHSHLSADGTLVCPKG 180
 Db 121 GRCRCPAGWRGDTCCSDVDECSARRGGCPQRCINTAGSYWCQCWEHSHLSADGTLVCPKG 180
 Qy 181 GPRVAPRPTGVDSAMKEEYORLQSRVYDLLEKQLVYIAPLHSLASQALHEHGLPDPGSL 240
 Db 181 GPRVAPRPTGVDSAMKEEYORLQSRVYDLLEKQLVYIAPLHSLASQALHEHGLPDPGSL 240
 Qy 241 VHSFQQLGRIDSLSEQISFLBEQLGSSCKKDS 273
 Db 241 VHSFQQLGRIDSLSEQISFLBEQLGSSCKKDS 273

RESULT 13
 US-09-978-188A-508
 Sequence 508, Application US/09978188A
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerltzen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gunney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Nadler, Mary A.
 APPLICANT: Pan, James J.
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2630P1C8
 CURRENT FILING DATE: 2001-10-15
 PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 2001-07-30
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/064249
 PRIOR FILING DATE: 1997-11-03
 PRIOR APPLICATION NUMBER: 60/065311
 PRIOR FILING DATE: 1997-11-13
 PRIOR APPLICATION NUMBER: 60/066364
 PRIOR FILING DATE: 1997-11-21
 PRIOR APPLICATION NUMBER: 60/077450

; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085580
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085573
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085704
 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/085697
 ; PRIOR FILING DATE: 1998-05-15

Query Match 100.0%; Score 1505; DB 25; Length 273;
 Best Local Similarity 100.0%; Pred. No. 4,6e-113;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSGQEVLLMMLVLAAGVGEHAYRPRRCVCAVRAHDDPVSESEVQVYVYPPFLTTCDGHR 60
 Db 1 MRSGQEVLLMMLVLAAGVGEHAYRPRRCVCAVRAHDDPVSESEVQVYVYPPFLTTCDGHR 60
 QY 61 ACSTYRTIYTAARSPGLAPAPRYAACCPGKRTSGLPGACGAAICQPPCRNNGSCVOP 120
 Db 61 ACSTYRTIYTAARSPGLAPAPRYAACCPGKRTSGLPGACGAAICQPPCRNNGSCVOP 120
 QY 121 GRGRCPAGWRDTCQSDVDECSARRGGCQPCRCINTAGSYWCQCEGHSLSDGTLCPKX 180
 Db 121 GRGRCPAGWRDTCQSDVDECSARRGGCQPCRCINTAGSYWCQCEGHSLSDGTLCPKX 180
 QY 181 GPPRVANPRTGVSAKKEVORLQSRVLLLEKLOLVLAHLSAQALEHGLPDRGSLI 240
 Db 181 GPPRVANPRTGVSAKKEVORLQSRVLLLEKLOLVLAHLSAQALEHGLPDRGSLI 240
 QY 241 VHSFOQLGRIDSLSQOISFLEBQIGSCCKKDS 273
 Db 241 VHSFOQLGRIDSLSQOISFLEBQIGSCCKKDS 273

RESULP 14
 US-09-978-189-506
 ; Sequence 506, Application US/09978189
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Geritlsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillam, Kenneth J.
 ; APPLICANT: Kljavin, Ivar J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2630PLC7
 ; CURRENT APPLICATION NUMBER: US/09/978,189
 ; PRIOR FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: 09/918585
 ; PRIOR FILING DATE: 2001-07-30

; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
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 ; PRIOR FILING DATE: 1997-11-21
 ; PRIOR APPLICATION NUMBER: 60/077450
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PRIOR FILING DATE: 1998-04-09
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 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085573
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697
 PRIOR FILING DATE: 1998-05-15

Query Match 100.0%; Score 1505; DB 25; Length 273;
 Best Local Similarity 100.0%; Pred. No. 4,6e-113;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSOEVLMMVLVLAIVGTEHAYRPGRRVCAVBAHGDVPSSEFVQRYVYQPFITTCGHR 60
 DB 1 MRGSOEVLMMVLVLAIVGTEHAYRPGRRVCAVBAHGDVPSSEFVQRYVYQPFITTCGHR 60
 QY 61 ACSTYRTTYRTAAYRSRPLAARPPRYACCPGMRKRTSGLPAGCGAATCQPPRNGSGCVQ 120
 DB 61 ACSTYRTTYRTAAYRSRPLAARPPRYACCPGMRKRTSGLPAGCGAATCQPPRNGSGCVQ 120
 QY 121 GRCCPAGMRGDTQSPVDECCSARRGGCPCRCINTAGSYWCQCMEGHSLSDADGTLCPKG 180
 DB 121 GRCCPAGMRGDTQSPVDECCSARRGGCPCRCINTAGSYWCQCMEGHSLSDADGTLCPKG 180
 QY 181 GPPVAVPPTGVDSAMKEEVORLQSRVDLLEKQLVLAIPLHSLASQALEHGLPDPGSL 240
 DB 181 GPPVAVPPTGVDSAMKEEVORLQSRVDLLEKQLVLAIPLHSLASQALEHGLPDPGSL 240
 QY 241 VHSFOQLGRIDLSLEQISFLEBOLGSCCKKDS 273
 DB 241 VHSFOQLGRIDLSLEQISFLEBOLGSCCKKDS 273

RESULT 15

US-09-978-189-508
 Sequence 508, Application US/09978189
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Deenoeyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gertlisen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Goddowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Kljavin, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel

```

APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC7
CURRENT APPLICATION NUMBER: US/09/978,199
PRIOR APPLICATION NUMBER: 2001-10-15
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
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Search completed: September 10, 2003, 17:23:05
Job time : 406 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 10, 2003, 17:15:18 ; Search time 61 Seconds
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Title: US-09-978-191a-506

Perfect score: 1505

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Searched: 541936 seqs, 145912426 residues

Total number of hits satisfying chosen parameters: 541936

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Post-Processing: Minimum Match 0%
Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1505	100.0	273	10 US-09-978-295A-506	Sequence 506, App
3	1505	100.0	273	10 US-09-978-295A-508	Sequence 508, App
4	1505	100.0	273	10 US-09-978-697-506	Sequence 506, App
5	1505	100.0	273	10 US-09-978-697-508	Sequence 508, App
6	1505	100.0	273	10 US-09-978-192A-506	Sequence 506, App
7	1505	100.0	273	10 US-09-978-192A-508	Sequence 508, App
8	1505	100.0	273	10 US-09-999-832A-506	Sequence 506, App
9	1505	100.0	273	10 US-09-999-832A-508	Sequence 508, App
10	1505	100.0	273	11 US-09-978-189-506	Sequence 506, App
11	1505	100.0	273	11 US-09-978-189-508	Sequence 508, App
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44	1505	100.0	273	12 US-09-978-188A-506	Sequence 506, App
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ALIGNMENTS

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; Sequence 10, Application US/09790264
; Parent No. US20020028508A1
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; APPLICANT: Goodearl, Andrew D.J.
; APPLICANT: McCarthy, Sean A.
; TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
; TITLE OF INVENTION: PROGNASTIC, DIAGNOSTIC, PREVENTIVE,
; TITLE OF INVENTION: THERAPEUTIC, AND OTHER
; FILE REFERENCE: 07334-322001
; CURRENT APPLICATION NUMBER: US/09/790,264
; PRIOR FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: US 09/065,661
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: US 09/298,531
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: US 09/065,363
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: US 09/124,538
; PRIOR FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 68
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; SEQ ID NO 10
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(22)
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Query Match 100.0%; Score 1505; DB 9; Length 273;
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RESULT 2

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 ? Sequence 506, Application US/09978295A
 ? Patent No. US20020156006A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Ashkenazi, Avi
 ? APPLICANT: Baker Kevin P.
 ? APPLICANT: Botstein, David
 ? APPLICANT: Desnoyers, Luc
 ? APPLICANT: Eaton, Dan
 ? APPLICANT: Ferrara, Napoleone
 ? APPLICANT: Filvaroff, Ellen
 ? APPLICANT: Fong, Sherman
 ? APPLICANT: Gao, Wei-Qiang
 ? APPLICANT: Gerber, Hanspeter
 ? APPLICANT: Gertlisen, Mary E.
 ? APPLICANT: Goddard, Audrey
 ? APPLICANT: Godowski, Paul J.
 ? APPLICANT: Grimaldi, J. Christopher
 ? APPLICANT: Gunney, Austin L.
 ? APPLICANT: Hillan, Kenneth J.
 ? APPLICANT: Kijavim, Var J.
 ? APPLICANT: Kuo, Sophia S.
 ? APPLICANT: Napier, Mary A.
 ? APPLICANT: Pan, James;
 ? APPLICANT: Paoni, Nicholas F.
 ? APPLICANT: Roy, Margaret Ann
 ? APPLICANT: Shelton, David L.
 ? APPLICANT: Stewart, Timothy A.
 ? APPLICANT: Tumas, Daniel
 ? APPLICANT: Williams, P. Mickey
 ? APPLICANT: Wood, William I.
 ? TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ? FILE REFERENCE: P2630P1C11
 ? CURRENT FILING DATE: 2001-10-15
 ? PRIOR APPLICATION NUMBER: 09/918585
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 PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1505; DB 10; Length 273;
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RESULT 3
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 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
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 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austen L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kijavitt, Ivar J.
 ; APPLICANT: Kud, Sophia S.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Naber, Mary A.
 ; APPLICANT: Pan, James
 ; APPLICANT: Paoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secured and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2630D1C11
 ; CURRENT APPLICATION NUMBER: US/09/978, 295A
 ; CURRENT FILING DATE: 2001-10-15
 ; PRIOR APPLICATION NUMBER: 09/918585

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 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1505; DB 10; Length 273;
 Best Local Similarity 100.0%; Pred. No. 1,5e-114;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 121 GRCRCPAWRGDTCCSDYDECSARRGGCPORCINTPAGSYWCQWEGHSLSDGTLVYRKG 180
 Qy 181 GPPRYVAPPTGVDSAMKEEYORLQSRVYDLAEKXQLVYAPVHSHASQALEHGLPDPSSL 240
 Db 181 GPPRYVAPPTGVDSAMKEEYORLQSRVYDLAEKXQLVYAPVHSHASQALEHGLPDPSSL 240
 Qy 241 VHSFQQLGRIDSLSBOISFLEEQLGSCSCKKDS 273
 Db 241 VHSFQQLGRIDSLSBOISFLEEQLGSCSCKKDS 273

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 ; Sequence 508, Application US/09978697
 ; Patent No. US20020169284A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Deenoyers, Luc
 ; APPLICANT: Eaton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
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 ; APPLICANT: Gutney, Austin L.

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 APPLICANT: Kijavim, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James.
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2630PIC27
 CURRENT APPLICATION NUMBER: US/09/978,697
 PRIOR APPLICATION NUMBER: 2001-10-16
 PRIOR FILING DATE: 2001-07-30
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PRIOR APPLICATION NUMBER: 60/085697

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Query Match      100.0%; Score 1505; DB 10; Length 273;
Best Local Similarity 100.0%; Pred. No. 1,5e-114;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 241 VHSFOQLGRIDSLSQISFLREQLGSCSCKKDS 273
DB 241 VHSFOQLGRIDSLSQISFLREQLGSCSCKKDS 273

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Patent No. US20020177553A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deshoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon

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APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
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APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C9
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CURRENT FILING DATE: 2001-10-15
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Query Match 100.0%; Score 1505; DB 10; Length 273;
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RESULT 7
 US-09-978-192A-508

Sequence 508. Application US/09978192A
 Patent No. US20020177553A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Deansoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
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 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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PRIOR APPLICATION NUMBER: 60/085573
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PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697

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Query Match 100.0% Score 1505; DB 10; Length 273;
 Best Local Similarity 100.0%; Pred. No. 1.5e-114;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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    1 MRGSEVLLMLLVAVGSTEHAHRGRVCAVRAHGDVSSFPVQVYQPELTTCDGHR 60
Db 1 MRGSEVLLMLLVAVGSTEHAHRGRVCAVRAHGDVSSFPVQVYQPELTTCDGHR 60
Oy 61 ACSRRTTYRTYRYSRPGIAPARPRYACCPGMRKRTSGLFPGACGAICPPCGNGSSCVOP 120
    61 .ACSTRYRTTYRYSRPGIAPARPRYACCPGMRKRTSGLFPGACGAICPPCGNGSSCVOP 120
Db 61 .ACSTRYRTTYRYSRPGIAPARPRYACCPGMRKRTSGLFPGACGAICPPCGNGSSCVOP 120
Oy 121 GRCRPAGMRGDTCCSDVDECSARRGGCPORCINTAGSYWCOCWESHSLADGTLCPVPG 180
    121 GRCRPAGMRGDTCCSDVDECSARRGGCPORCINTAGSYWCOCWESHSLADGTLCPVPG 180
Db 121 GRCRPAGMRGDTCCSDVDECSARRGGCPORCINTAGSYWCOCWESHSLADGTLCPVPG 180
Oy 181 GPRVAVNPTGVDSAMKEEVQRLQSRVDLLEKLDVLAPLHSLASQALEHGLPDPGSL 240
    181 GPRVAVNPTGVDSAMKEEVQRLQSRVDLLEKLDVLAPLHSLASQALEHGLPDPGSL 240

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Db 181 GPRVAVNPTGVDSAMKEEVQRLQSRVDLLEKLDVLAPLHSLASQALEHGLPDPGSL 240
Oy 241 VHSFOOLGRIDLSRQISFLEROLGSCGCKXD 273
    241 VHSFOOLGRIDLSRQISFLEROLGSCGCKXD 273
Db 241 VHSFOOLGRIDLSRQISFLEROLGSCGCKXD 273

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RESULT 8
 US-09-999-832A-506

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; Sequence 506, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavlin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
TITLE OF INVENTION: Selected and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630PIC63
CURRENT FILING DATE: 2001-10-24
PRIOR FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
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 / PRIOR APPLICATION NUMBER: 60/085697

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Db 61 ACSYRTTIVRTAYRRRPPGLAPRPRVACCPGKMTSGLGACGAAICQPPCRNGSGCVQP 120
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 Db 241 VHSFOQLGRIDLSLSEQISFLERQLGSCCKXDS 273
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 / Sequence 508, Application US/09999832A
 / Publication No. US20020192706A1
 / GENERAL INFORMATION:
 / APPLICANT: Ashkenazi, Avi
 / APPLICANT: Baker Kevin P.
 / APPLICANT: Botstein, David
 / APPLICANT: Desnoyers, Luc
 / APPLICANT: Eaton, Dan
 / APPLICANT: Ferrara, Napoleone
 / APPLICANT: Filvaroff, Ellen
 / APPLICANT: Fong, Sherman
 / APPLICANT: Gao, Wei-Qiang
 / APPLICANT: Gerber, Hanspeter
 / APPLICANT: Gerritsen, Mary E.
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 / APPLICANT: Gurney, Austin L.
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 / APPLICANT: Pan, James
 / APPLICANT: Paoni, Nicholas F.
 / APPLICANT: Roy, Margaret Ann
 / APPLICANT: Shelton, David L.
 / APPLICANT: Stewart, Timothy A.
 / APPLICANT: Tumas, Daniel
 / APPLICANT: Williams, P. Mickey
 / APPLICANT: Wood, William I.
 / TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 / FILE REFERENCE: P2630PIC63
 / CURRENT APPLICATION NUMBER: US/09/999, 832A
 / CURRENT FILING DATE: 2001-10-24
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 / PRIOR FILING DATE: 2001-07-30
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 ; PRIOR APPLICATION NUMBER: 60/085697

Query Match 100.0%; Score 1505; DB 11; Length 273;
 Best Local Similarity 100.0%; Pred. No. 1,5e-114;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 MRGSOEVLMLVLAAGGTEHAYRPGRRVAVAHDDPSESEVQVYQPLITTCGRH 60
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 Db 61 ACSTYRTTYRTRAYRRSPGLAPARPRVACCPGKRTSGLPACGAIICQPPCRNGGSCVCP 120
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 QY 181 GPPVAVNPITGVDSAMKEEVQRLQSRVYDLLEKQLVLAAPHSIASQALEHGLPDDGSLI 240
 Db 181 GPPVAVNPITGVDSAMKEEVQRLQSRVYDLLEKQLVLAAPHSIASQALEHGLPDDGSLI 240
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 Db 241 VHSFOQLGRIDLSLEQISFLEBQIGSCCKKDS 273

RESULT 11

US-09-978-189-508
 ; Sequence 508, Application US/09978189
 ; Publication No. US20030004102A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi
 ; APPLICANT: Baker Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Denoyers, Luc
 ; APPLICANT: Baton, Dan
 ; APPLICANT: Ferrara, Napoleon
 ; APPLICANT: Filvaroff, Ellen
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Gao, Wei-Qiang
 ; APPLICANT: Gerber, Hanspeter
 ; APPLICANT: Gerritsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Hillan, Kenneth J.
 ; APPLICANT: Kijavich, Ivair J.
 ; APPLICANT: Kuo, Sophia S.
 ; APPLICANT: Napier, Mary A.
 ; APPLICANT: Pan, James;
 ; APPLICANT: Peoni, Nicholas F.
 ; APPLICANT: Roy, Margaret Ann
 ; APPLICANT: Shelton, David L.
 ; APPLICANT: Stewart, Timothy A.
 ; APPLICANT: Tumas, Daniel
 ; APPLICANT: Williams, P. Mickey
 ; APPLICANT: Wood, William I.
 ; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 ; FILE REFERENCE: P2630P1C7
 ; CURRENT APPLICATION NUMBER: US/09/978,189
 ; CURRENT FILING DATE: 2001-10-15
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 Sequence 506, Application US/09978608A
 Publication No. US20030045462A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Kljavin, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel


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; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
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; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-978-585A-506

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Best Local Similarity 100.0%; Pred. No. 1.5e-114;
Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Inc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
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; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kljavin, Ivar J.
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; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2630P1C15
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Job time : 63 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

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(without alignments)
398.306 Million cell updates/sec

Title: US-09-978-191A-506

Perfect score: 1505

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Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
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Listing first 45 summaries

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*Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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; Patent No. 6392018
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Yeung, George
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; TITLE OF INVENTION: LIVER SPLEEN
; FILE REFERENCE: 24011-727
; CURRENT APPLICATION NUMBER: US/09/249,697A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 08/968,800
; PRIOR FILING DATE: 1997-11-22
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(553)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-249-697A-6

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; 58 KGVIC-EATCEPGCK-FGECVGNKRCRCPFGYGTGKTCSDVNECGMKRPRCQHRCVNTHGS 115
; 159 YWCQCEHGSLSADGTLV-----PKGGPP-----RVAPN 188
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; Sequence 6, Application US/09363316B
; Patent No. 6392019
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Yeung, George
; TITLE OF INVENTION: EGF MOTIF PROTEIN MATERIALS AND METHODS
; FILE REFERENCE: 28110/35852
; CURRENT APPLICATION NUMBER: US/09/363,316B
; CURRENT FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: US 09/249,697
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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (357)
; OTHER INFORMATION: Xaa = any amino acid
US-09-363-316B-6

```

```

Query Match          16.9%; Score 254.5; DB 4; Length 553;
Best Local Similarity 34.5%; Pred. No. 1.4e-12;
Matches 60; Conservative 21; Mismatches 62; Indels 31; Gaps 7;
QY 39 PVESEFQRYVYQPLTTCDDGHRACSTYRTYRTRARRRSPGLAAPPARYACCPGKRTSGL 98
; 2 PLPWSIALPFLPLPWVAGFGNMAASARHGHGLASA--RQPGVCHYGTKEACCVGMRRNS-- 57
; 99 PGACGAATCQPPCRNGGSCVQPGRCRCPAGWRGDTQSDVDECSARRGGGPPRCINTAGS 158
; 58 KGVIC-EATCEPGCK-FGECVGNKRCRCPFGYGTGKTCSDVNECGMKRPRCQHRCVNTHGS 115
; 159 YWCQCEHGSLSADGTLV-----PKGGPP-----RVAPN 188
; 116 YKCFCLSGHMLMPDAD-CVNSRTCAMINCOYSCEDTEBEGPQCLCPSSGRLAPN 168
; DB
; US-09-363-316B-6
; Sequence 6, Application US/09363316B
; Patent No. 6392019
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Yeung, George
; TITLE OF INVENTION: EGF MOTIF PROTEIN MATERIALS AND METHODS
; FILE REFERENCE: 28110/35852
; CURRENT APPLICATION NUMBER: US/09/363,316B
; CURRENT FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: US 09/249,697
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 08/968,800
; PRIOR FILING DATE: 1997-11-22
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (357)
; OTHER INFORMATION: Xaa = any amino acid
US-09-363-316B-6

```

```

DB 2 PLPWSIALPFLPLPWVAGFGNMAASARHGHGLASA--RQPGVCHYGTKEACCVGMRRNS-- 57
QY 99 PGACGAATCQPPCRNGGSCVQPGRCRCPAGWRGDTQSDVDECSARRGGGPPRCINTAGS 158
; 58 KGVIC-EATCEPGCK-FGECVGNKRCRCPFGYGTGKTCSDVNECGMKRPRCQHRCVNTHGS 115
QY 159 YWCQCEHGSLSADGTLV-----PKGGPP-----RVAPN 188
; 116 YKCFCLSGHMLMPDAD-CVNSRTCAMINCOYSCEDTEBEGPQCLCPSSGRLAPN 168
; DB

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RESULT 4
; Sequence 389, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 389
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Mouse
US-09-312-283C-389

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Query Match          16.8%; Score 252.5; DB 4; Length 284;
Best Local Similarity 36.3%; Pred. No. 9.3e-13;
Matches 53; Conservative 15; Mismatches 51; Indels 27; Gaps 4;
QY 66 RTIYRTRARRRSPGLAAPPARYACCPGKRTSGLPGACGAATCQPPCRNGGSCVQPGRCRC 125
; 47 RDIYRTRARRRSPGLAAPPARYACCPGKRTSGLPGACGAATCQPPCRNGGSCVQPGRCRC 102
QY 126 PAGWRGDTQSDVDECSARRGGGPPRCINTAGSYWCQCEHGS----- 169
; 103 PFGYGTGKTCSDVNECGMKRPRCQHRCVNTHGSYKCFCLSGHMLLPDATCSNSRTCARIN 162
QY 170 -----SADGTLVCPKGGPPRVAPN 188
; 163 QYSCEDTEBEGPQCLCPSSGRLAPN 188
; DB

```

```

RESULT 5
; Sequence 19, Application US/09249697A
; Patent No. 6392018
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Yeung, George
; TITLE OF INVENTION: NOVEL EGF MOTIF PROTEIN OBTAINED FROM A CDNA LIBRARY OF FETAL
; TITLE OF INVENTION: LIVER SPLEEN
; FILE REFERENCE: 24011-727
; CURRENT APPLICATION NUMBER: US/09/249,697A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 08/968,800
; PRIOR FILING DATE: 1997-11-22
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-249-697A-19

```



```

US-09-363-316B-4
; Sequence 4, Application US/09363316B
; Patent No. 6392019
; GENERAL INFORMATION:
; APPLICANT: Yeung, George
; APPLICANT: Ford, John
; TITLE OF INVENTION: EGF MOTIF PROTEIN MATERIALS AND METHODS
; FILE REFERENCE: 28110/35852
; CURRENT APPLICATION NUMBER: US/09/363, 316B
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: US 09/249,697
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 08/968,800
; PRIOR FILING DATE: 1997-11-22
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 537
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (503)
; OTHER INFORMATION: Xaa = any amino acid
US-09-363-316B-4

```

```

Query Match          14.3%; Score 216.5; DB 4; Length 537;
Best Local Similarity 39.3%; Pred. No. 1,4e-09;
Matches 48; Conservative 10; Mismatches 35; Indels 29; Gaps 6;

QY 91 GMRRTSGLPAGCAATCQPPCRNGSCVQPGRCRCPAGMRGDTQSDVDECSARRGGCPQ 150
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 GMRRTS--KGVC-EATCEPCK-FGEVGVGNKRCRCFPGYTKTCSQDVNHECCMKRPPCQH 56
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 151 RCINTAGSYWCQCEWGHSLSDGTLV-----PKGAPP-----RVA 186
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 57 RCVNTHSYKCFCLSGHMLMPDAT-CVNSRTCAMINCOVSCEDTBEQPOCLCPSSGLRFLA 115
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 187 PN 188
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 116 PN 117
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

RESULT 10
US-09-249-697A-3
; Sequence 3, Application US/09249697A
; Patent No. 6392018
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Yeung, George
; TITLE OF INVENTION: NOVEL EGF MOTIF PROTEIN OBTAINED FROM A CDNA LIBRARY OF FETAL
; FILE REFERENCE: 24011-727
; CURRENT APPLICATION NUMBER: US/09/249,697A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 08/968,800
; PRIOR FILING DATE: 1997-11-22
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-249-697A-3

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```

Query Match          14.3%; Score 215.5; DB 4; Length 100;
Best Local Similarity 48.3%; Pred. No. 2,5e-10;
Matches 42; Conservative 8; Mismatches 32; Indels 5; Gaps 4;

QY 91 GMRRTSGLPAGCAATCQPPCRNGSCVQPGRCRCPAGMRGDTQSDVDECSARRGGCPQ 150
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 GMRRTS--KGVC-EATCEPCK-FGEVGVGNKRCRCFPGYTKTCSQDVNHECCMKRPPCQH 56
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

QY 151 RCINTAGSYWCQCEWGHSLSDGTLV 177
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 57 RCVNTHSYKCFCLSGHMLMPDAT-CV 82
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

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RESULT 11
US-09-363-316B-3
; Sequence 3, Application US/09363316B
; Patent No. 6392019
; GENERAL INFORMATION:
; APPLICANT: Ford, John
; APPLICANT: Yeung, George
; TITLE OF INVENTION: EGF MOTIF PROTEIN MATERIALS AND METHODS
; FILE REFERENCE: 28110/35852
; CURRENT APPLICATION NUMBER: US/09/363, 316B
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: US 09/249,697
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 08/968,800
; PRIOR FILING DATE: 1997-11-22
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 100
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-363-316B-3

```

```

Query Match          14.3%; Score 215.5; DB 4; Length 100;
Best Local Similarity 48.3%; Pred. No. 2,5e-10;
Matches 42; Conservative 8; Mismatches 32; Indels 5; Gaps 4;

QY 91 GMRRTSGLPAGCAATCQPPCRNGSCVQPGRCRCPAGMRGDTQSDVDECSARRGGCPQ 150
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 GMRRTS--KGVC-EATCEPCK-FGEVGVGNKRCRCFPGYTKTCSQDVNHECCMKRPPCQH 56
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 151 RCINTAGSYWCQCEWGHSLSDGTLV 177
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 57 RCVNTHSYKCFCLSGHMLMPDAT-CV 82
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

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RESULT 12
US-09-467-997-1
; Sequence 1, Application US/09467997
; Patent No. 6379925
; GENERAL INFORMATION:
; APPLICANT: Kitajewski, Jan
; APPLICANT: Uytendaele, Hendrik
; TITLE OF INVENTION: ANGIOGENIC MODULATION BY NOTCH SIGNAL TRANSDUCTION
; FILE REFERENCE: 53863-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/467,997
; PRIOR FILING DATE: 1999-12-20
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1964
; TYPE: PRT
; ORGANISM: mouse
US-09-467-997-1

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Query Match          13.0%; Score 196; DB 4; Length 1964;
Best Local Similarity 34.2%; Pred. No. 2,7e-07;
Matches 50; Conservative 12; Mismatches 54; Indels 30; Gaps 7;

QY 80 APPARRYACCPGK-RTSGLPAGCAATCQPPCRNGSCVQPG--RCRCPAGMRGDTQ 135
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 134 ASGRPQSCBPGWGBOCQQRDRCSA-----NPCANGGVCIATYPOIQCRCPGFEHGTCE 189
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 136 SDVDECSARRGGCPQ--RCINTAGSYWCQ---WEGHSLSDGTLV-----KGGPRVA 186
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 190 RDINECTLEBFPQPDQGTSCNHTLGSYQCLCPVGVQBGPPCKLRKAGCPSSCLNGGTCQLV 249
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 187 PNP-----TGVDAMKEE 199
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Db 250 PEGHSTFHLCLPPEGTGLDCENMPD 275

RESULT 13

US-08-282-141-2

Sequence 2, Application US/08282141

Patent No. 5538861

GENERAL INFORMATION:

APPLICANT: Schneider, Claudio

APPLICANT: Varnum, Brian

APPLICANT: Avanzi, Giancarlo

APPLICANT: Brancolini, Claudio

APPLICANT: Manfioletti, Guidalberto

TITLE OF INVENTION: Stimulating Factor for the AXL Receptor

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Amgen Inc.

STREET: 1840 Dehavilland Drive

CITY: Thousand Oaks

STATE: California

COUNTRY: United States

ZIP: 91320-1789

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/282,141

FILING DATE:

CLASSIFICATION: 435

INFORMATION FOR SEQ. ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 678 amino acids

TYPE: amino acid

STRANDEDNESS: unknown

TOPOLOGY: unknown

MOLECULE TYPE: protein

US-08-282-141-2

Query Match 12.6%; Score 189; DB 1; Length 678;

Best Local Similarity 34.2%; Pred. No. 2.9e-07;

Matches 53; Conservative 8; Mismatches 64; Indels 30; Gaps 8;

Qy 46 QRVYQPLTTCGH-----RACSTYRTIYTRAVRSPGLAPARRRYACC-----PGWK 93

Db 47 RRAFOVFEBAKQGHLEKRECVBELCS--REBARVEVFNDEPDTDFYRPRYLDCINKYGSPT 104

Qy 94 RTSG-----LPGACGAALICQPPC-RNGGSCVQP--GR--CRCPAGMRGDTCCQSDVDEC 141

Db 105 KNSGPAATCVQNLPPDC---TNPFCDRKGTQACQDLMGNFPLCLCRAGMGRLCDKDVNVC 160

Qy 142 SARRGCCPQRCINTAGSYWCQCQWEGHSLSDGTLIC 176

Db 161 SQENGGCLQICHNKKGSFHCSSGSEFELSSDGRTC 195

RESULT 14

US-08-435-434-2

Sequence 2, Application US/08435434

Patent No. 5714385

GENERAL INFORMATION:

APPLICANT: Mather, Jennie P.

APPLICANT: Li, Ronghao

APPLICANT: Chen, Jian

TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/435,434

FILING DATE: 10-MAY-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

ATTORNEY/AGENT INFORMATION:

NAME: Lee, Wendy M.

REGISTRATION NUMBER: 00,000

REFERENCE/DOCKET NUMBER: 946-2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-1994

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ. ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 678 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-435-434-2

Query Match 12.6%; Score 189; DB 1; Length 678;

Best Local Similarity 34.2%; Pred. No. 2.9e-07;

Matches 53; Conservative 8; Mismatches 64; Indels 30; Gaps 8;

Qy 46 QRVYQPLTTCGH-----RACSTYRTIYTRAVRSPGLAPARRRYACC-----PGWK 93

Db 47 RRAFOVFEBAKQGHLEKRECVBELCS--REBARVEVFNDEPDTDFYRPRYLDCINKYGSPT 104

Qy 94 RTSG-----LPGACGAALICQPPC-RNGGSCVQP--GR--CRCPAGMRGDTCCQSDVDEC 141

Db 105 KNSGPAATCVQNLPPDC---TNPFCDRKGTQACQDLMGNFPLCLCRAGMGRLCDKDVNVC 160

Qy 142 SARRGCCPQRCINTAGSYWCQCQWEGHSLSDGTLIC 176

Db 161 SQENGGCLQICHNKKGSFHCSSGSEFELSSDGRTC 195

RESULT 15

US-08-435-436-2

Sequence 2, Application US/08435436

Patent No. 5721139

GENERAL INFORMATION:

APPLICANT: Mather, Jennie P.

APPLICANT: Li, Ronghao

APPLICANT: Chen, Jian

TITLE OF INVENTION: ISOLATING AND CULTURING SCHWANN CELLS

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/435,436

FILING DATE: 10-MAY-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

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APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 00,000
REFERENCE/DOCKET NUMBER: 946-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1994
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 678 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-435-436-2

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Query Match 12.6%; Score 189; DB 1; Length 678;
Best Local Similarity 34.2%; Pred. No. 2.9e-07;
Matches 53; Conservative 8; Mismatches 64; Indels 30; Gaps 8;

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QY 46 QRYVQPLLTCDGH-----RAGSTYRTTYRTAYRRSPGLAPARPRYACC-----PGWK 93
Db 47 RRAFQVEBAKQGHLEKRECVHELCS--REARREVENDPPTDYFYPRYLDCINKYGSPTY 104
QY 94 RTSG-----LPGACGAALICQPPC--RNGGSCVQP--GR--CRCPAGMRGDTCQSDVDEC 141
Db 105 KNSGFATCVQNLPPQC-----TPNPCDRKGTQACODLMDGNFFCLCKAGMGRSLCDKXDVNEC 160
QY 142 SARRGCPQRCINTAGSYWCQCWEGHSLADGTLG 176
Db 161 SOENGGCLQICHNKPQSFHCSCHSGFELSSDGRTG 195

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Search completed: September 10, 2003, 17:16:13
Job time : 30 secs

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PR 20-MAR-1998; 98US-0078939.
 PR 25-MAR-1998; 98US-0079294.
 PR 26-MAR-1998; 98US-0079656.
 PR 27-MAR-1998; 98US-0079663.
 PR 27-MAR-1998; 98US-0079664.
 PR 27-MAR-1998; 98US-0079689.
 PR 27-MAR-1998; 98US-0079728.
 PR 27-MAR-1998; 98US-0079786.
 PR 30-MAR-1998; 98US-0079920.
 PR 30-MAR-1998; 98US-0079923.
 PR 31-MAR-1998; 98US-0080105.
 PR 31-MAR-1998; 98US-0080107.
 PR 31-MAR-1998; 98US-0080155.
 PR 31-MAR-1998; 98US-0080194.
 PR 01-APR-1998; 98US-0080327.
 PR 01-APR-1998; 98US-0080328.
 PR 01-APR-1998; 98US-0080333.
 PR 01-APR-1998; 98US-0080334.
 PR 08-APR-1998; 98US-0081049.
 PR 08-APR-1998; 98US-0081070.
 PR 08-APR-1998; 98US-0081071.
 PR 09-APR-1998; 98US-0081195.
 PR 09-APR-1998; 98US-0081203.
 PR 09-APR-1998; 98US-0081329.
 PR 15-APR-1998; 98US-0081817.
 PR 15-APR-1998; 98US-0081838.
 PR 15-APR-1998; 98US-0081952.
 PR 15-APR-1998; 98US-0081955.
 PR 21-APR-1998; 98US-0082568.
 PR 21-APR-1998; 98US-0082569.
 PR 22-APR-1998; 98US-0082700.
 PR 22-APR-1998; 98US-0082704.
 PR 22-APR-1998; 98US-0082804.
 PR 23-APR-1998; 98US-0082767.
 PR 23-APR-1998; 98US-0082796.
 PR 27-APR-1998; 98US-0083336.
 PR 28-APR-1998; 98US-0083322.
 PR 29-APR-1998; 98US-0083392.
 PR 29-APR-1998; 98US-0083495.
 PR 29-APR-1998; 98US-0083496.
 PR 29-APR-1998; 98US-0083499.
 PR 29-APR-1998; 98US-0083500.
 PR 29-APR-1998; 98US-0083545.
 PR 29-APR-1998; 98US-0083554.
 PR 29-APR-1998; 98US-0083558.
 PR 29-APR-1998; 98US-0083559.
 PR 30-APR-1998; 98US-0083742.
 PR 05-MAY-1998; 98US-0084366.
 PR 06-MAY-1998; 98US-0084414.
 PR 06-MAY-1998; 98US-0084441.
 PR 07-MAY-1998; 98US-0084598.
 PR 07-MAY-1998; 98US-0084600.
 PR 07-MAY-1998; 98US-0084627.
 PR 07-MAY-1998; 98US-0084637.
 PR 07-MAY-1998; 98US-0084639.
 PR 07-MAY-1998; 98US-0084640.
 PR 07-MAY-1998; 98US-0084643.
 PR 13-MAY-1998; 98US-0085323.
 PR 13-MAY-1998; 98US-0085338.
 PR 13-MAY-1998; 98US-0085539.
 PR 15-MAY-1998; 98US-0085573.
 PR 15-MAY-1998; 98US-0085579.
 PR 15-MAY-1998; 98US-0085580.
 PR 15-MAY-1998; 98US-0085589.
 PR 15-MAY-1998; 98US-0085822.
 PR 15-MAY-1998; 98US-0085889.
 PR 15-MAY-1998; 98US-0085697.
 PR 15-MAY-1998; 98US-0085700.
 PR 15-MAY-1998; 98US-0085704.
 PR 18-MAY-1998; 98US-0086023.
 PR 22-MAY-1998; 98US-0086114.
 PR 22-MAY-1998; 98US-0086430.
 PR 22-MAY-1998; 98US-0086486.

PR 28-MAY-1998; 98US-0087098.
 PR 28-MAY-1998; 98US-0087106.
 PR 28-MAY-1998; 98US-0087208.
 PR 30-JUL-1998; 98US-0094651.
 PR 11-SEP-1998; 98US-0100038.
 XX
 PA (GENE) GENENTECH INC.
 XX
 PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
 XX
 DR WPI: 1999-551358/46.
 DR N-PSDB: AA234311.
 XX
 PS New secreted and transmembrane polypeptides and their polynucleotides,
 PT useful for treating blood coagulation disorders, cancers and cellular
 PR adhesion disorders
 XX
 XX Claim 12; Fig 213; 530pp; English.
 CC The present invention describes secreted and transmembrane polypeptides
 CC and their polynucleotides. The nucleotide sequences are useful as
 CC sources of probes, primers, for chromosome mapping, and for generation
 CC of antisense sequences. They can also be used to create transgenic
 CC animals. The proteins can be used to treat a variety of diseases and
 CC disorders, depending on their function. Diseases that may be treated
 CC include blood coagulation disorders, cancers and cellular adhesion
 CC disorders. They may also be used to raise antibodies. AA233891 to
 CC AA234318, and AA41685 to AA41774 represent polynucleotide and
 CC polypeptide sequence given in the exemplification of the present
 XX invention.
 XX
 SQ Sequence 273 AA:
 Query Match 100.0%; Score 1505; DB 20; Length 273;
 Best Local Similarity 100.0%; Pred. No. 5.5e-95;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MRGSEVLLMVLVLAIVGTEHAYRPGRRVCAVAHAGDPVSESRVORVYOBFLTCCGHR 60
 Db 1 MRGSEVLLMVLVLAIVGTEHAYRPGRRVCAVAHAGDPVSESRVORVYOBFLTCCGHR 60
 OY 61 ACSTYRTIYRTAYRRSPGLAPARPRVYACCPGMRKTSGLPGAAGAIICPPCRNGSSCVOP 120
 Db 61 ACSTYRTIYRTAYRRSPGLAPARPRVYACCPGMRKTSGLPGAAGAIICPPCRNGSSCVOP 120
 OY 121 GRCRPAGWRBDTQOSVDDECSARRGGCPQRCINTAGSYWCQMEGHSLSADGTLCPVKG 180
 Db 121 GRCRPAGWRBDTQOSVDDECSARRGGCPQRCINTAGSYWCQMEGHSLSADGTLCPVKG 180
 OY 181 GPPRYAPRPTGVDSAMKEVORLQSRVLDLBEKTLQVLVAPLHSLASQALEHGLPDPSSL 240
 Db 181 GPPRYAPRPTGVDSAMKEVORLQSRVLDLBEKTLQVLVAPLHSLASQALEHGLPDPSSL 240
 OY 241 VHSFQQLGRIDSLSEQISFLEEQLGSCSCCKKDS 273
 Db 241 VHSFQQLGRIDSLSEQISFLEEQLGSCSCCKKDS 273
 RESULT 2
 AA41770
 ID AA41770 standard; Protein: 273 AA.
 AC AA41770;
 DT 07-DEC-1999 (first entry)
 XX
 XX Human PRO1330 protein sequence.
 KM Human; PRO: EST: expressed sequence tag; PCR primer; hybridisation;
 KM probe; blood coagulation disorder; cancer; cellular adhesion disorder;
 KM secreted protein; transmembrane protein.
 XX
 OS Homo sapiens.

XX WO9946281-A2.
 XX 16-SEP-1999.
 XX 08-MAR-1999; 99WO-US05028.
 XX 10-MAR-1998; 98US-0077450.
 PR 11-MAR-1998; 98US-0077632.
 PR 11-MAR-1998; 98US-0077641.
 PR 11-MAR-1998; 98US-0077649.
 PR 12-MAR-1998; 98US-0077791.
 PR 13-MAR-1998; 98US-0078004.
 PR 17-MAR-1998; 98US-0040220.
 PR 20-MAR-1998; 98US-0078886.
 PR 20-MAR-1998; 98US-0078910.
 PR 20-MAR-1998; 98US-0078936.
 PR 20-MAR-1998; 98US-0078939.
 PR 20-MAR-1998; 98US-0079294.
 PR 25-MAR-1998; 98US-0079656.
 PR 26-MAR-1998; 98US-0079663.
 PR 27-MAR-1998; 98US-0079664.
 PR 27-MAR-1998; 98US-0079689.
 PR 27-MAR-1998; 98US-0079728.
 PR 27-MAR-1998; 98US-0079786.
 PR 30-MAR-1998; 98US-0079920.
 PR 30-MAR-1998; 98US-0079923.
 PR 31-MAR-1998; 98US-0080105.
 PR 31-MAR-1998; 98US-0080107.
 PR 31-MAR-1998; 98US-0080165.
 PR 31-MAR-1998; 98US-0080194.
 PR 01-APR-1998; 98US-0080327.
 PR 01-APR-1998; 98US-0080328.
 PR 01-APR-1998; 98US-0080333.
 PR 01-APR-1998; 98US-0080334.
 PR 08-APR-1998; 98US-0081049.
 PR 08-APR-1998; 98US-0081070.
 PR 08-APR-1998; 98US-0081071.
 PR 09-APR-1998; 98US-0081195.
 PR 09-APR-1998; 98US-0081203.
 PR 09-APR-1998; 98US-0081229.
 PR 15-APR-1998; 98US-0081817.
 PR 15-APR-1998; 98US-0081838.
 PR 15-APR-1998; 98US-0081952.
 PR 15-APR-1998; 98US-0081955.
 PR 21-APR-1998; 98US-0082568.
 PR 21-APR-1998; 98US-0082569.
 PR 22-APR-1998; 98US-0082700.
 PR 22-APR-1998; 98US-0082704.
 PR 22-APR-1998; 98US-0082704.
 PR 23-APR-1998; 98US-0082767.
 PR 23-APR-1998; 98US-0082796.
 PR 27-APR-1998; 98US-0083336.
 PR 28-APR-1998; 98US-0083322.
 PR 29-APR-1998; 98US-0083392.
 PR 29-APR-1998; 98US-0083495.
 PR 29-APR-1998; 98US-0083496.
 PR 29-APR-1998; 98US-0083499.
 PR 29-APR-1998; 98US-0083500.
 PR 29-APR-1998; 98US-0083545.
 PR 29-APR-1998; 98US-0083554.
 PR 29-APR-1998; 98US-0083558.
 PR 29-APR-1998; 98US-0083559.
 PR 30-APR-1998; 98US-0083742.
 PR 05-MAY-1998; 98US-0084366.
 PR 05-MAY-1998; 98US-0084414.
 PR 06-MAY-1998; 98US-0084441.
 PR 07-MAY-1998; 98US-0084598.
 PR 07-MAY-1998; 98US-0084600.
 PR 07-MAY-1998; 98US-0084627.
 PR 07-MAY-1998; 98US-0084637.
 PR 07-MAY-1998; 98US-0084639.
 PR 07-MAY-1998; 98US-0084640.

PR 07-MAY-1998; 98US-0084643.
 PR 13-MAY-1998; 98US-0085323.
 PR 13-MAY-1998; 98US-0085338.
 PR 13-MAY-1998; 98US-0085339.
 PR 15-MAY-1998; 98US-0085573.
 PR 15-MAY-1998; 98US-0085579.
 PR 15-MAY-1998; 98US-0085580.
 PR 15-MAY-1998; 98US-0085582.
 PR 15-MAY-1998; 98US-0085689.
 PR 15-MAY-1998; 98US-0085697.
 PR 15-MAY-1998; 98US-0085700.
 PR 15-MAY-1998; 98US-0085704.
 PR 18-MAY-1998; 98US-0086023.
 PR 22-MAY-1998; 98US-0086392.
 PR 22-MAY-1998; 98US-0086414.
 PR 22-MAY-1998; 98US-0086430.
 PR 22-MAY-1998; 98US-0086486.
 PR 28-MAY-1998; 98US-0087098.
 PR 28-MAY-1998; 98US-0087106.
 PR 30-JUL-1998; 98US-0087208.
 PR 11-SEP-1998; 98US-0094651.
 PR 11-SEP-1998; 98US-0100038.
 XX (GETH) GENENTECH INC.
 XX Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
 XX WPI, 1999-551358/46.
 XX N-PSDB; AAZ34312.
 DR New secreted and transmembrane polypeptides and their polynucleotides,
 XX useful for treating blood coagulation disorders, cancers and cellular
 XX adhesion disorders -
 XX PT
 XX Claim 12; Fig 215; 530pp; English.
 PS The present invention describes secreted and transmembrane polypeptides
 XX and their polynucleotides. The nucleotide sequences are useful as
 XX sources of probes, primers, for chromosome mapping, and for generation
 XX of antisense sequences. They can also be used to create transgenic
 XX animals. The proteins can be used to treat a variety of diseases and
 XX disorders, depending on their function. Diseases that may be treated
 XX include blood coagulation disorders, cancers and cellular adhesion
 XX disorders. They may also be used to raise antibodies. AAZ33891 to
 XX AAZ34338, and AA41685 to AA41774 represent polynucleotide and
 XX polypeptide sequence given in the exemplification of the present
 XX invention.
 CC
 CC Sequence 273 AA;
 SQ
 Query Match 100.0%; Score 1505; DB 20; Length 273;
 Best Local Similarity 100.0%; Pred. No. 5,5e-95;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRGSOEVLMLWLVAVGGTEHAYRPGRRVCAVAHGDPPSESVORVYOPFLTTCCGHR 60
 Db 1 MRGSOEVLMLWLVAVGGTEHAYRPGRRVCAVAHGDPPSESVORVYOPFLTTCCGHR 60
 OY 61 ACSTYRTTYRTRAYRSRSPGLAPARPRVACCPGMRKTSGLPGACGALICQPPCRNGSCVOP 120
 Db 61 ACSTYRTTYRTRAYRSRSPGLAPARPRVACCPGMRKTSGLPGACGALICQPPCRNGSCVOP 120
 OY 121 GRCRCPAGMRGDTQGSVDDECSARAGGCPQRCINTTASGYWCQCGEHSLSADGTLCPVKG 180
 Db 121 GRCRCPAGMRGDTQGSVDDECSARAGGCPQRCINTTASGYWCQCGEHSLSADGTLCPVKG 180
 OY 181 GPPRVAANPPTGVSAKMEEVORLQSRVDLLEBKLOLVLAFLHSLASQALSHGLPDPSSL 240
 Db 181 GPPRVAANPPTGVSAKMEEVORLQSRVDLLEBKLOLVLAFLHSLASQALSHGLPDPSSL 240
 OY 241 VHSFQOLGRIDLSLEQISFLEBQVGSCKKDS 273
 Db 241 VHSFQOLGRIDLSLEQISFLEBQVGSCKKDS 273

RESULT 3
 AAB44325
 ID AAB44325 standard; Protein; 273 AA.
 XX
 XX AAB44325;
 AC
 DT 08-FEB-2001 (first entry)
 XX
 DE Human PRO213-1 protein sequence SEQ ID NO:506.
 XX
 KM Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;
 XX expressed sequence tag; detection; cancer.
 OS Homo sapiens.
 XX
 PN WO200053756-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 18-FEB-2000; 2000WO-US04341.
 XX
 PR 08-MAR-1999; 99WO-US05028.
 XX 12-MAR-1999; 99US-0123957.
 PR 29-MAR-1999; 99US-0126773.
 PR 21-APR-1999; 99US-0130232.
 PR 28-APR-1999; 99US-0131445.
 PR 14-MAY-1999; 99US-0134287.
 PR 23-JUN-1999; 99US-0141037.
 PR 26-JUL-1999; 99US-0145698.
 PR 29-OCT-1999; 99US-0162506.
 PR 30-NOV-1999; 99WO-US28313.
 PR 02-DEC-1999; 99WO-US28551.
 PR 16-DEC-1999; 99WO-US30095.
 PR 30-DEC-1999; 99WO-US31243.
 PR 05-JAN-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 XX
 XX (GENTECH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DJ,
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Garber H, Gerritsen ME,
 PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ,
 PI Kijavini IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA,
 PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI,
 DR WPI; 2000-611443/58.
 DR N-PSDB; AAC78585.
 XX
 PT Novel PRO polypeptides and polynucleotides used in detection methods,
 PT to target bioactive molecules to specific cells, and to modulate
 PT cellular activities -
 XX
 PS Claim 12; Fig 213; 636pp; English.
 XX
 CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed
 CC sequence tag) sequences which encode secreted or transmembrane PRO
 CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic
 CC activity. The polynucleotides and polypeptides can be used for detecting
 CC the presence of PRO polypeptides in samples, for linking bioactive
 CC molecules to cells and for modulating biological activities of cells.
 CC using the polypeptides for specific targeting. The polypeptide targeting
 CC can be used to kill the target cells, e.g. for the treatment of cancers.
 CC The polypeptide pairs provide specific targeting of bioactive molecules
 CC to cells. AAC78600 to AAC78897 represent PCR primers and probes used in
 CC the isolation of the PRO polynucleotide sequences.
 CC
 CC Sequence 273 AA;

Query Match 100.0%; Score 1505; DB 21; Length 273;
 Best Local Similarity 100.0%; Pred. No. 5.5e-95;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSEVLLMVLVLAANGTEHAHYRGRVAVRAPHGPPVSEFPQRYVOPPLTTCDGHR 60
 DB 1 MRGSEVLLMVLVLAANGTEHAHYRGRVAVRAPHGPPVSEFPQRYVOPPLTTCDGHR 60

QY 61 ACSYRRTTYRTRRSPGIAAPRPRYACCPGWRKRTSGIPGACGAALICPPRCNGSSCYQP 120
 DB 61 ACSYRRTTYRTRRSPGIAAPRPRYACCPGWRKRTSGIPGACGAALICPPRCNGSSCYQP 120

QY 121 GRCRCPAGWRGDTCCSDVDECGARRGGCCPQRCINTAGSYWCQCEHSHLSADGTLVCPKG 180
 DB 121 GRCRCPAGWRGDTCCSDVDECGARRGGCCPQRCINTAGSYWCQCEHSHLSADGTLVCPKG 180

QY 181 GPPRYVAPNPTGVDSAMKREVRVLRVLDLBEKLOLVIAAPRHSLSAQLAHEGLDPGSL 240
 DB 181 GPPRYVAPNPTGVDSAMKREVRVLRVLDLBEKLOLVIAAPRHSLSAQLAHEGLDPGSL 240

QY 241 VHSFOQLGRIDSLSEQISFLEBOLGSCSCKKDS 273
 DB 241 VHSFOQLGRIDSLSEQISFLEBOLGSCSCKKDS 273

RESULT 4
 AAB44326
 ID AAB44326 standard; Protein; 273 AA.
 XX
 XX AAB44326;
 AC
 DT 08-FEB-2001 (first entry)
 XX
 DE Human PRO1330 protein sequence SEQ ID NO:508.
 XX
 KM Human; secreted protein; transmembrane protein; PRO; EST; cytostatic;
 XX expressed sequence tag; detection; cancer.
 OS Homo sapiens.
 XX
 PN WO200053756-A2.
 XX
 PD 14-SEP-2000.
 XX
 PF 18-FEB-2000; 2000WO-US04341.
 XX
 PR 08-MAR-1999; 99WO-US05028.
 XX 12-MAR-1999; 99US-0123957.
 PR 29-MAR-1999; 99US-0126773.
 PR 21-APR-1999; 99US-0130232.
 PR 28-APR-1999; 99US-0131445.
 PR 14-MAY-1999; 99US-0134287.
 PR 23-JUN-1999; 99US-0141037.
 PR 26-JUL-1999; 99US-0145698.
 PR 29-OCT-1999; 99US-0162506.
 PR 30-NOV-1999; 99WO-US28313.
 PR 02-DEC-1999; 99WO-US28551.
 PR 16-DEC-1999; 99WO-US30095.
 PR 30-DEC-1999; 99WO-US31243.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 XX
 XX (GENTECH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DJ,
 PI Ferrara N, Filvaroff E, Fong S, Gao W, Garber H, Gerritsen ME,
 PI Goddard A, Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ,
 PI Kijavini IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA,
 PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI,
 DR WPI; 2000-611443/58.
 DR N-PSDB; AAC78585.
 XX
 PT Novel PRO polypeptides and polynucleotides used in detection methods,
 PT to target bioactive molecules to specific cells, and to modulate
 PT cellular activities -
 XX
 PS Claim 12; Fig 213; 636pp; English.
 XX
 CC AAC78458 to AAC78599 represent polynucleotide and EST (expressed
 CC sequence tag) sequences which encode secreted or transmembrane PRO
 CC polypeptides. The PRO polynucleotides and polypeptides have cytostatic
 CC activity. The polynucleotides and polypeptides can be used for detecting
 CC the presence of PRO polypeptides in samples, for linking bioactive
 CC molecules to cells and for modulating biological activities of cells.
 CC using the polypeptides for specific targeting. The polypeptide targeting
 CC can be used to kill the target cells, e.g. for the treatment of cancers.
 CC The polypeptide pairs provide specific targeting of bioactive molecules
 CC to cells. AAC78600 to AAC78897 represent PCR primers and probes used in
 CC the isolation of the PRO polynucleotide sequences.
 CC
 CC Sequence 273 AA;

DR WPI; 2000-611443/58.
 N-PSDB; AAC78586.
 Novel PRO polypeptides and polynucleotides used in detection methods,
 to target bioactive molecules to specific cells, and to modulate
 cellular activities -
 Claim 12; Fig 215; 636pp; English.
 AAC78458 to AAC78599 represent polynucleotide and EST (expressed
 sequence tag) sequences which encode secreted or transmembrane PRO
 polypeptides. The PRO polynucleotides and polypeptides have cytotoxic
 activity. The polynucleotides and polypeptides can be used for detecting
 the presence of PRO polypeptides in samples, for linking bioactive
 molecules to cells and for modulating biological activities of cells,
 using the polypeptides for specific targeting. The polypeptide targeting
 can be used to kill the target cells, e.g. for the treatment of cancers.
 CC The polypeptide pairs provide specific targeting of bioactive molecules
 CC to cells. AAC78600 to AAC78997 represent PCR primers and probes used in
 CC the isolation of the PRO polynucleotide sequences.
 CC
 CC Sequence 273 AA:

Query Match 100.0%; Score 1505; DB 21; Length 273;
 Best Local Similarity 100.0%; Pred. No. 5,5e-95;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRGSOEVLMMWLVLA VGGTEHA YRPRGAVRAHGDVSESFVORYOPELTTCDGHR 60
 DB 1 MRGSOEVLMMWLVLA VGGTEHA YRPRGAVRAHGDVSESFVORYOPELTTCDGHR 60
 OY 61 ACSTYRTTYRTRAYRRSPGLA PARPRYACCPGMRKRTSGLPGACGAAICQPPCRNGSSCVQP 120
 DB 61 ACSTYRTTYRTRAYRRSPGLA PARPRYACCPGMRKRTSGLPGACGAAICQPPCRNGSSCVQP 120
 OY 121 GRCRCPAGWRGDTCCSDVDNDCSARRGGCFCORCINTINGSYWCCQEGHSISADGTLCPKRG 180
 DB 121 GRCRCPAGWRGDTCCSDVDNDCSARRGGCFCORCINTINGSYWCCQEGHSISADGTLCPKRG 180
 OY 181 GPPRYVAPNPTGVDSANKKEVORLQSRVDLLEKLDQVLA PLRSLASQALEHGLPDRGSL 240
 DB 181 GPPRYVAPNPTGVDSANKKEVORLQSRVDLLEKLDQVLA PLRSLASQALEHGLPDRGSL 240
 OY 241 VHSFOQLGRIDSLSEQISFLERQLSGSCCKKDS 273
 DB 241 VHSFOQLGRIDSLSEQISFLERQLSGSCCKKDS 273

RESULT 5
 AAB18673
 ID AAB18673 standard; Protein; 273 AA.
 XX
 AC AAB18673;
 XX
 DT 22-JAN-2001 (first entry)
 XX
 DE Amino acid sequence of a human a PRO213 polypeptide.
 XX
 KM Growth arrest-specific gene 6 protein homologue; PRO320; PRO938; PRO1031;
 KM PRO296; PRO213; PRO1449; angiogenesis; cardiovascularisation; PRO1330;
 KM cardiovascular disorder; endothelial disorder; angiogenic disorder;
 KM cancer; trauma; wound; atherosclerosis; cardiac hypertrophy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FH Peptide 1..19
 FT /note= "signal sequence"
 FT Modified-site 19..25
 FT /note= "N-myristoylation site"
 FT Modified-site 26..30
 FT /note= "amidation site"
 FT Modified-site 78..84

FT /note= "N-myristoylation site"
 FT Modified-site 93..97
 FT /note= "cAMP- and GMP-dependent protein kinase
 FT phosphorylation site"
 FT Modified-site 97..103
 FT /note= "N-myristoylation site"
 FT Modified-site 100..106
 FT /note= "N-myristoylation site"
 FT Modified-site 103..109
 FT /note= "N-myristoylation site"
 FT Region 123..135
 FT /note= "EGF-like domain cysteine pattern signature"
 FT Region 130..133
 FT /note= "cell attachment sequence"
 FT Modified-site 152..164
 FT /note= "aspartic acid and asparagine hydroxylation site"
 FT Modified-site 157..163
 FT /note= "N-myristoylation site"
 FT Modified-site 191..197
 FT /note= "N-myristoylation site"
 FT Modified-site 265..271
 FT /note= "N-myristoylation site"

Query Match 100.0%; Score 1505; DB 21; Length 273;
 Best Local Similarity 100.0%; Pred. No. 5,5e-95;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MRGSOEVLMMWLVLA VGGTEHA YRPRGAVRAHGDVSESFVORYOPELTTCDGHR 60
 DB 1 MRGSOEVLMMWLVLA VGGTEHA YRPRGAVRAHGDVSESFVORYOPELTTCDGHR 60
 OY 61 ACSTYRTTYRTRAYRRSPGLA PARPRYACCPGMRKRTSGLPGACGAAICQPPCRNGSSCVQP 120
 DB 61 ACSTYRTTYRTRAYRRSPGLA PARPRYACCPGMRKRTSGLPGACGAAICQPPCRNGSSCVQP 120

30-DEC-1999; 99WO-US31274.
 08-MAR-1999; 99WO-US05028.
 21-APR-1999; 99US-0130232.
 26-APR-1999; 99US-0131022.
 28-APR-1999; 99US-0131445.
 14-MAY-1999; 99US-0134287.
 02-DEC-1999; 99WO-US28565.
 (GENTH) GENENTECH INC.
 Baker KP, Ferrara N, Goddard A, Gurney AL, Hillan KJ, Williams PM,
 Wood WT;
 WPI; 2000-638138/61.
 N-PSDB; AAA5702.
 A composition useful for treatment and diagnosis of a cardiovascular,
 endothelial or angiogenic disorder, especially cancer, comprises (an
 agonist or antagonist of) a PRO320, PRO938, PRO1031, PRO296, PRO213,
 PRO1330 or PRO1449 polypeptide -
 Claim 67; Fig 10; 152pp; English.
 The present sequence represents PRO213, a human growth arrest-specific
 gene 6 protein homologue. The specification describes PRO320, PRO938,
 PRO1031, PRO296, PRO213, and PRO1449 polypeptides. The
 polypeptides promoter or inhibit angiogenesis and cardiovascularisation
 in mammals. The polypeptides are used for the treatment and diagnosis
 of a cardiovascular, endothelial or angiogenic disorder, especially
 cancer. Disorders that can be diagnosed, treated or prevented by
 the polypeptides of the invention include trauma such as wounds,
 atherosclerosis, and cardiac hypertrophy.
 Sequence 273 AA:

Db 61 ACSTYRTTYRTAVYRRKSPGLAPARPRRYACCPGKRTSGILPGAGAAICQPPCRNNGSSCVQP 120
 QY 121 GRRCPCPAGMRGPTCCSDVDECSARRRGGCRPCINTAGSYWCQWEGHSLSDADGTLCPYK 180
 Db 121 GRRCPCPAGMRGPTCCSDVDECSARRRGGCRPCINTAGSYWCQWEGHSLSDADGTLCPYK 180
 QY 181 GPPRYAHPPTGVDSAMKEEVORLQSRVDLLEBKQLVLAAPLHSLASQALHEHGLPDPGSL 240
 Db 181 GPPRYAHPPTGVDSAMKEEVORLQSRVDLLEBKQLVLAAPLHSLASQALHEHGLPDPGSL 240
 QY 241 VHSFQQLGRIDSLSEQISFLLEQIGSGSCCKKDS 273
 Db 241 VHSFQQLGRIDSLSEQISFLLEQIGSGSCCKKDS 273
 RESULT 6
 AAB18674 ID AAB18674 standard; Protein: 273 AA.
 AC AAB18674;
 XX 22-JAN-2001 (first entry)
 DT
 XX
 DE Amino acid sequence of a human PRO1330 polypeptide.
 XX
 KW Notch 4 homologue; PRO320; PRO938; PRO1031; PRO296; PRO213; PRO1449;
 KW angiogenesis; cardiovascularisation; PRO1330; cardiovascular disorder;
 KW endothelial disorder; angiogenic disorder; cancer; trauma; wound;
 KW atherosclerosis; cardiac hypertrophy.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FH Peptide 1..19
 FT /note= "signal sequence"
 FT 19..25
 FT /note= "N-myristoylation site"
 FT 26..30
 FT /note= "amidation site"
 FT 78..84
 FT /note= "N-myristoylation site"
 FT 93..97
 FT /note= "CaM- and GMP-dependent protein kinase
 FT phosphorylation site"
 FT 97..103
 FT /note= "N-myristoylation site"
 FT 100..106
 FT /note= "N-myristoylation site"
 FT 103..109
 FT /note= "N-myristoylation site"
 FT 123..135
 FT /note= "EGF-like domain cysteine pattern signature"
 FT 130..133
 FT /note= "cell attachment sequence"
 FT 152..164
 FT /note= "aspartic acid and asparagine hydroxylation site"
 FT 157..163
 FT /note= "N-myristoylation site"
 FT 191..197
 FT /note= "N-myristoylation site"
 FT 255..271
 FT /note= "N-myristoylation site"
 FT
 XX
 XX WO200053752-A2.
 XX
 PD 14-SBP-2000.
 XX
 PD 30-DEC-1999; 99WO-US31274.
 XX
 PF 08-MAR-1999; 99WO-US05028.
 XX
 PR 21-APR-1999; 99US-0130232.
 XX
 PR 26-APR-1999; 99US-0131022.
 XX
 PR 28-APR-1999; 99US-0131445.

PR 14-MAY-1999; 99US-0134287.
 PR 02-DEC-1999; 99WO-US28565.
 PA (GENENTECH INC.
 XX
 PI Baker KP, Ferrara N, Goddard A, Gurney AL, Hillian KJ, Williams PM;
 PI Wood WI;
 XX
 DR WPI; 2000-638138/61.
 DR N-PSDB; AAAV5703.
 XX
 XX
 PT A composition useful for treatment and diagnosis of a cardiovascular,
 PT endothelial or angiogenic disorder, especially cancer, comprises (an
 PT agonist or antagonist of) a PRO320, PRO938, PRO1031, PRO296, PRO213,
 PT PRO1330 or PRO1449 polypeptide -
 XX
 XX
 PS Claim 67; Fig 12; 152pp; English.
 XX
 XX
 CC The present sequence represents PRO1330, a human notch 4 homologue.
 CC The specification describes PRO320, PRO938, PRO1031, PRO296, PRO213,
 CC PRO1330 and PRO1449 polypeptides. The polypeptides promoter or
 CC inhibit angiogenesis and cardiovascularisation in mammals. The
 CC polypeptides are used for the treatment and diagnosis of a
 CC cardiovascular, endothelial or angiogenic disorder, especially
 CC cancer. Disorders that can be diagnosed, treated or prevented by
 CC the polypeptides of the invention include trauma such as wounds,
 CC atherosclerosis, and cardiac hypertrophy.
 XX
 XX
 SQ Sequence 273 AA;
 Query Match 100.0%; Score 1505; DB 21; Length 273;
 Best Local Similarity 100.0%; Pred. No. 5,5e-95;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRGSEVLIIMLVAVGCTHAYRPGRRVCAVRAHGDVSESFVQRYVQPLFTTCDGHR 60
 Db 1 MRGSEVLIIMLVAVGCTHAYRPGRRVCAVRAHGDVSESFVQRYVQPLFTTCDGHR 60
 QY 61 ACSTYRTTYRTAVYRRSPGLAPARPRRYACCPGKRTSGILPGAGAAICQPPCRNNGSSCVQP 120
 Db 61 ACSTYRTTYRTAVYRRSPGLAPARPRRYACCPGKRTSGILPGAGAAICQPPCRNNGSSCVQP 120
 QY 121 GRRCPCPAGMRGPTCCSDVDECSARRRGGCRPCINTAGSYWCQWEGHSLSDADGTLCPYK 180
 Db 121 GRRCPCPAGMRGPTCCSDVDECSARRRGGCRPCINTAGSYWCQWEGHSLSDADGTLCPYK 180
 QY 181 GPPRYAHPPTGVDSAMKEEVORLQSRVDLLEBKQLVLAAPLHSLASQALHEHGLPDPGSL 240
 Db 181 GPPRYAHPPTGVDSAMKEEVORLQSRVDLLEBKQLVLAAPLHSLASQALHEHGLPDPGSL 240
 QY 241 VHSFQQLGRIDSLSEQISFLLEQIGSGSCCKKDS 273
 Db 241 VHSFQQLGRIDSLSEQISFLLEQIGSGSCCKKDS 273
 RESULT 7
 AAB24042 ID AAB24042 standard; Protein: 273 AA.
 XX
 XX AAB24042;
 DT 25-JAN-2001 (first entry)
 XX
 DE Human PRO213 protein sequence SEQ ID NO:4.
 XX
 KW Human; tumour; diagnosis; neoplastic disease; identification; cancer;
 KW tumorigenesis; detection; neoplastic cell growth; proliferation;
 KW cytostatic; antiinflammatory; immunomodulatory; inflammatory disorder;
 KW immunological disorder.
 XX
 OS Homo sapiens.
 XX
 XX WO200053754-A1.

XX 14-SEP-2000.
 PD 06-JAN-2000; 2000MO-US00277.
 PF 08-MAR-1999; 99WO-US05028.
 PR 12-MAR-1999; 99US-0123957.
 PR 29-MAR-1999; 99US-0126773.
 PR 21-APR-1999; 99US-0130232.
 PR 28-APR-1999; 99US-0131445.
 PR 05-OCT-1999; 99WO-US23089.
 PR 30-NOV-1999; 99WO-US28313.
 PR 02-DEC-1999; 99WO-US28551.
 PR 30-DEC-1999; 99WO-US28564.
 PR 30-DEC-1999; 99WO-US31243.
 XX 30-DEC-1999; 99WO-US31274.
 XX (GETH) GENENTECH INC.
 XX Baker KP, Desauvage FU, Goddard A, Gurney AL, Klein RD, Roy MA;
 PI Wood WI;
 XX WPI: 2000-572269/53.
 DR N-PSDB; AAC58226.
 XX
 PT New isolated antibody for use in compositions and methods for the
 PT diagnosis and treatment of neoplastic cell growth and proliferation in
 PT mammals, including humans, and in monitoring tumor treatment -
 XX
 PS Claim 61; Fig 4; 195pp; English.
 XX
 CC The present invention describes an isolated antibody (Ab) that binds to
 CC one of the human proteins (P) designated PRO213, PRO1330, PRO1449,
 CC PRO324, PRO351, PRO362, PRO615, PRO531, PRO3664, PRO618,
 CC PRO772, PRO703, PRO792 or PRO474. The Ab can be used in compositions
 CC and methods for the diagnosis and treatment of neoplastic cell growth
 CC and proliferation in mammals, including humans. Genes and polypeptides
 CC encoded by them, that are amplified in the genome of a tumour cell, can
 CC be identified and are useful targets for the treatment and prevention of
 CC certain cancers and may be used to monitor tumour treatment. Compounds
 CC that inhibit the expression or activity of the identified polypeptides
 CC can be identified and used as antagonists. Benign or malignant tumours,
 CC inflammatory disorders and immunological disorders can be treated.
 CC AAC58123 to AAC58224 represent hybridisation probes and PCR primers used
 CC in the isolation of the human PRO sequences. AAC58225 to AAC58241 and
 CC AAB24041 to AAB24056 represent human PRO polynucleotide and protein
 CC sequences given in the exemplification of the present invention.
 CC
 CC Sequence 273 AA;
 SO

Query Match 100.0%; Score 1505; DB 21; Length 273;
 Best Local Similarity 100.0%; Pred. No. 5.5e-95;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MRGSEVLLMLLVLA VGGTETHAYRGRVCAVRAHGDVPSSEFVQRYVYQPLTTCDDGHR 60
 DB 1 MRGSEVLLMLLVLA VGGTETHAYRGRVCAVRAHGDVPSSEFVQRYVYQPLTTCDDGHR 60
 OY 61 ACSYRTTYRTYRYSRPGIAPRPRRYACCPGKWRKRSGLFGACGAALICPPPCNGSSCVQP 120
 DB 61 ACSYRTTYRTYRYSRPGIAPRPRRYACCPGKWRKRSGLFGACGAALICPPPCNGSSCVQP 120
 OY 121 GRCRCPAGMRDPTCCSDVDEGASARRGGGCFORCINTTAGSYWCCWBSHSLSAUGTLCVPRKG 180
 DB 121 GRCRCPAGMRDPTCCSDVDEGASARRGGGCFORCINTTAGSYWCCWBSHSLSAUGTLCVPRKG 180
 OY 181 GPPRVAVPNTGVDASAMKEVORLQSRVLDLLEKTLQIVLAPLHSLASQALEHGIAPPGSIL 240
 DB 181 GPPRVAVPNTGVDASAMKEVORLQSRVLDLLEKTLQIVLAPLHSLASQALEHGIAPPGSIL 240
 OY 241 VHSFOOLGRIDLSLEQISFLEROLGSSGCKKDS 273
 DB 241 VHSFOOLGRIDLSLEQISFLEROLGSSGCKKDS 273

RESULT 8
 AAB24043
 ID AAB24043 standard; Protein; 273 AA.
 XX
 AC AAB24043;
 XX
 DT 25-JAN-2001 (first entry)
 XX
 DE Human PRO1330 protein sequence SEQ ID NO:6.
 XX
 KW Human; tumour; diagnosis; neoplastic disease; identification; cancer;
 KW tumorigenesis; detection; neoplastic cell growth; proliferation;
 KW cytostatic; antiinflammatory; immunomodulatory; inflammatory disorder;
 KW immunological disorder.
 XX
 OS Homo sapiens.
 OS
 XX WO200053754-A1.
 XX
 PN 14-SEP-2000.
 XX
 PD 06-JAN-2000; 2000MO-US00277.
 XX
 PF 08-MAR-1999; 99WO-US05028.
 XX
 PR 12-MAR-1999; 99US-0123957.
 PR 29-MAR-1999; 99US-0126773.
 PR 21-APR-1999; 99US-0130232.
 PR 28-APR-1999; 99US-0131445.
 PR 05-OCT-1999; 99WO-US23089.
 PR 30-NOV-1999; 99WO-US28313.
 PR 02-DEC-1999; 99WO-US28551.
 PR 30-DEC-1999; 99WO-US28564.
 PR 30-DEC-1999; 99WO-US31243.
 PR 30-DEC-1999; 99WO-US31274.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Desauvage FU, Goddard A, Gurney AL, Klein RD, Roy MA;
 PI Wood WI;
 XX WPI: 2000-572269/53.
 DR N-PSDB; AAC58227.
 XX
 PT New isolated antibody for use in compositions and methods for the
 PT diagnosis and treatment of neoplastic cell growth and proliferation in
 PT mammals, including humans, and in monitoring tumor treatment -
 XX
 PS Claim 61; Fig 6; 195pp; English.
 XX
 CC The present invention describes an isolated antibody (Ab) that binds to
 CC one of the human proteins (P) designated PRO213, PRO1330, PRO1449,
 CC PRO324, PRO351, PRO362, PRO615, PRO531, PRO3664, PRO618,
 CC PRO772, PRO703, PRO792 or PRO474. The Ab can be used in compositions
 CC and methods for the diagnosis and treatment of neoplastic cell growth
 CC and proliferation in mammals, including humans. Genes and polypeptides
 CC encoded by them, that are amplified in the genome of a tumour cell, can
 CC be identified and are useful targets for the treatment and prevention of
 CC certain cancers and may be used to monitor tumour treatment. Compounds
 CC that inhibit the expression or activity of the identified polypeptides
 CC can be identified and used as antagonists. Benign or malignant tumours,
 CC inflammatory disorders and immunological disorders can be treated.
 CC AAC58123 to AAC58224 represent hybridisation probes and PCR primers used
 CC in the isolation of the human PRO sequences. AAC58225 to AAC58241 and
 CC AAB24041 to AAB24056 represent human PRO polynucleotide and protein
 CC sequences given in the exemplification of the present invention.
 CC
 CC Sequence 273 AA;
 SO

Query Match 100.0%; Score 1505; DB 21; Length 273;
 Best Local Similarity 100.0%; Pred. No. 5.5e-95;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MRGSEVLLMLLVLA VGGTETHAYRGRVCAVRAHGDVPSSEFVQRYVYQPLTTCDDGHR 60
 DB 1 MRGSEVLLMLLVLA VGGTETHAYRGRVCAVRAHGDVPSSEFVQRYVYQPLTTCDDGHR 60
 OY 61 ACSYRTTYRTYRYSRPGIAPRPRRYACCPGKWRKRSGLFGACGAALICPPPCNGSSCVQP 120
 DB 61 ACSYRTTYRTYRYSRPGIAPRPRRYACCPGKWRKRSGLFGACGAALICPPPCNGSSCVQP 120
 OY 121 GRCRCPAGMRDPTCCSDVDEGASARRGGGCFORCINTTAGSYWCCWBSHSLSAUGTLCVPRKG 180
 DB 121 GRCRCPAGMRDPTCCSDVDEGASARRGGGCFORCINTTAGSYWCCWBSHSLSAUGTLCVPRKG 180
 OY 181 GPPRVAVPNTGVDASAMKEVORLQSRVLDLLEKTLQIVLAPLHSLASQALEHGIAPPGSIL 240
 DB 181 GPPRVAVPNTGVDASAMKEVORLQSRVLDLLEKTLQIVLAPLHSLASQALEHGIAPPGSIL 240
 OY 241 VHSFOOLGRIDLSLEQISFLEROLGSSGCKKDS 273
 DB 241 VHSFOOLGRIDLSLEQISFLEROLGSSGCKKDS 273

QY 1 MRGSOEVLMMMLVLAAGTETHAYRPPRRVCAVPAHGDVSESEFVQRYVYOPFLTTCDGHR 60
 Db 1 MRGSOEVLMMMLVLAAGTETHAYRPPRRVCAVPAHGDVSESEFVQRYVYOPFLTTCDGHR 60
 QY 61 ACSTYRTITRTAYRRSPGLAPARPRYACCPGMRKRTSGLPAGCGAALICOPPRNGSGCVQP 120
 Db 61 ACSTYRTITRTAYRRSPGLAPARPRYACCPGMRKRTSGLPAGCGAALICOPPRNGSGCVQP 120
 QY 121 GRRCPCPAGMRGDDTQOSVDDECSARRGGCPORCINTAGSSWQCWEGHSLSDGTLTLPVCKG 180
 Db 121 GRRCPCPAGMRGDDTQOSVDDECSARRGGCPORCINTAGSSWQCWEGHSLSDGTLTLPVCKG 180
 QY 181 GPPRYAHPPTGVDAMKEEVRQLQSRVLDLEBKQLVLAAPHSIASQALHEGLPDPGSL 240
 Db 181 GPPRYAHPPTGVDAMKEEVRQLQSRVLDLEBKQLVLAAPHSIASQALHEGLPDPGSL 240
 QY 241 VHSFQQLGRIDLSLEQISFLBEQIGSGSCCKKDS 273
 Db 241 VHSFQQLGRIDLSLEQISFLBEQIGSGSCCKKDS 273

RESULT 9

AA952137
 ID AA952137 standard; Protein: 273 AA.
 AC AA952137;
 XX
 DT 01-FEB-2000 (first entry)
 DE Human TANGO 125 (T125) amino acid sequence.
 XX
 KW TANGO 125; T125; alternative splice variant; EGF domain; antibody;
 KM secreted protein; agonist; antagonist; predictive medicine; treatment;
 KW forensic biology.
 XX
 OS Homo sapiens.
 FH Key
 FT Peptide
 FT 1..22 Location/Qualifiers
 FT /label= signal_peptide
 FT 23..274
 FT /label= TANGO_125
 FT 107..134
 FT /note= "EGF-like domain 1"
 FT 141..176
 FT /note= "EGF-like domain 2"
 XX
 PN MO9954437-A2.
 XX
 PD 28-OCT-1999.
 XX
 PF 23-APR-1999; 99WO-US089900.
 XX
 PR 23-APR-1998; 98US-0065363.
 PR 23-APR-1999; 99US-0065363.
 XX
 PA (MILL-) MILLENNIUM BIOTHERAPEUTICS INC.
 PI Holtzman DA;
 XX
 DR WPI: 2000-013240/01.
 DR N-PSDB; AA237131.
 XX
 PT Novel polynucleotides and polypeptides used to modulate a variety of
 PT cellular processes
 XX
 PS Claim 1; Fig 1; 120pp; English.
 CC
 CC This is the human TANGO 125 (T125) amino acid sequence. The T125 protein
 CC has two epidermal growth factor (EGF)-like domains at amino acids
 CC 107-134 and 141-176 and is predicted to have a molecular weight of
 CC approximately 30kD. T125 is predicted to have no transmembrane domains

CC and appears to be a secreted protein. There are three alternatively
 CC spliced forms of the T125 gene: T125a, T125b and T125c (AA237132-237135).
 CC The sequences of all variants of T125 are used in the invention to create
 CC antibodies which selectively bind to T125. The T125 polypeptide is used
 CC to modulate a variety of cellular processes. It can be used to produce
 CC fusion proteins. The protein may also be used to produce antibodies, and
 CC to identify T125 antagonists and agonists. The T125 polynucleotides,
 CC polypeptides, homologues and antibodies can be used in screening assays;
 CC predictive medicine; and methods of treatment of T125 associated
 CC disorders. The T125 polynucleotides can be used to express the protein;
 CC to detect T125 mRNA; to detect genetic alterations in the T125 gene; in
 CC forensic biology; and as a source of primers and probes.
 XX
 SQ Sequence 273 AA;
 QY Query Match 100.0%; Score 1505; DB 21; Length 273;
 Db Best Local Similarity 100.0%; Pred. No. 5.5e-95;
 QY Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 1 MRGSOEVLMMMLVLAAGTETHAYRPPRRVCAVPAHGDVSESEFVQRYVYOPFLTTCDGHR 60
 QY 61 ACSTYRTITRTAYRRSPGLAPARPRYACCPGMRKRTSGLPAGCGAALICOPPRNGSGCVQP 120
 Db 61 ACSTYRTITRTAYRRSPGLAPARPRYACCPGMRKRTSGLPAGCGAALICOPPRNGSGCVQP 120
 QY 121 GRRCPCPAGMRGDDTQOSVDDECSARRGGCPORCINTAGSSWQCWEGHSLSDGTLTLPVCKG 180
 Db 121 GRRCPCPAGMRGDDTQOSVDDECSARRGGCPORCINTAGSSWQCWEGHSLSDGTLTLPVCKG 180
 QY 181 GPPRYAHPPTGVDAMKEEVRQLQSRVLDLEBKQLVLAAPHSIASQALHEGLPDPGSL 240
 Db 181 GPPRYAHPPTGVDAMKEEVRQLQSRVLDLEBKQLVLAAPHSIASQALHEGLPDPGSL 240
 QY 241 VHSFQQLGRIDLSLEQISFLBEQIGSGSCCKKDS 273
 Db 241 VHSFQQLGRIDLSLEQISFLBEQIGSGSCCKKDS 273

RESULT 10
 AA921079
 ID AA921079 standard; Protein: 273 AA.
 AC AA921079;
 XX
 DT 01-JUL-2002 (first entry)
 DE Human T125 (TANGO-125) protein.
 XX
 KW Human; haematopoiesis; clotting; kidney failure; wound healing; cancer;
 KW neoplasia; pancreatic disorder; pancreatitis; cerebrovascular disease;
 KW heart disorder; ischaemic heart disease; neuroprotective; vulnary;
 KW cardiovascular disorder; ischaemic heart disease; immunosuppressive;
 KW glomerular disease; glomerulonephritis; uterine disorder; hyperplasia;
 KW fetal spleen; prostate disorder; inflammatory disease; Crohn's disease;
 KW proliferative disorder; gynaecological; haemostatic; antibacterial;
 KW systemic lupus erythematosus; immunodeficiency disorder; antisthmatic;
 KW cytostatic; nephrotoxic; antidiabetic; cerebroprotective; tranquilliser;
 KW hypotensive; tumour; injury; trauma; antiangiinal; vasotropic; antifungal;
 KW apoptotic disorder; rheumatoid arthritis; cardiac; renal disorder;
 KW hepatotropic; antiproliferative; antiallergic; dermatological; vituicide;
 T125.
 XX
 OS Homo sapiens.
 FH Key
 FT Peptide
 FT 1..22 Location/Qualifiers
 FT /label= signal_peptide
 FT 23..273
 FT /note= "Human mature T125 protein"
 FT 107..134
 FT /note= "Epidermal growth factor domain 1"
 FT Domain

PT useful for treating a PRO related disorder and for diagnosing tumours
 PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
 PT tumour or liver tumour -
 XX Claim 11; Figure 178; 359pp; English.
 XX
 CC The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
 CC agonists and antagonists are useful for treating a PRO related disorder.
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression, in pericyte cells, for stimulating
 CC the proliferation or differentiation of chondrocyte cells, for
 CC stimulating the release of tumour necrosis factor-alpha from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,
 CC and in chromosome and gene mapping. AA083592-AA083713 represent human PRO
 CC protein sequences of the invention.
 CC
 XX Sequence 273 AA;

Query Match. 100.0%; Score 1505; DB 23; Length 273;
 Best Local Similarity 100.0%; Pred. No. 5,5e-95;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSGQVLLMMLVLAAGVTEHAYRPGRRVCAVRAHGDPPVSESFVQRYQPFLLTCDGHR 60
 Db 1 MRGSGQVLLMMLVLAAGVTEHAYRPGRRVCAVRAHGDPPVSESFVQRYQPFLLTCDGHR 60
 QY 61 ACSTYRTIYRTAARBSGGLAPARPRVACCPGWRKTSGLPACGAAICOPPCRNNGSCVQP 120
 Db 61 ACSTYRTIYRTAARBSGGLAPARPRVACCPGWRKTSGLPACGAAICOPPCRNNGSCVQP 120
 QY 121 GRGCRPAGWRGDTQSDVDDECSARRGCCPQRCINTAGSYWCCQMEGHSLSADDTLCPVPGK 180
 Db 121 GRGCRPAGWRGDTQSDVDDECSARRGCCPQRCINTAGSYWCCQMEGHSLSADDTLCPVPGK 180
 QY 181 GPRPVAHPPTGVDSAMKEVQRIQSRVDLIEEKLQVLAFLHSLASQALHEGLPDPGSLI 240
 Db 181 GPRPVAHPPTGVDSAMKEVQRIQSRVDLIEEKLQVLAFLHSLASQALHEGLPDPGSLI 240
 QY 241 VHSFQQLGRIDSLSEQISFLERDLGSCCKKDS 273
 Db 241 VHSFQQLGRIDSLSEQISFLERDLGSCCKKDS 273

RESULT 12
 ABU61155
 ID ABU61155 standard; Protein; 273 AA.

AC ABU61155;
 DT 08-MAY-2003 (First entry)
 XX
 DE Human PRO213-1 polypeptide.

XX Human; PRO polypeptide; secreted and transmembrane protein;
 KW Immune disorder; diabetes; hyper-insulinaemia; hypo-insulinaemia;
 KW Cardiac insufficiency; nervous system disorder; kidney disorder;
 KW bone disorder; cartilage disorder; arthritis; tumour; wound healing;
 KW genetic disorder; cytoskeletal; antidiabetic; antiinflammatory;
 KW antiarthritic; anti-tumour; vulnerrary; antiinflammatory; dermatological;
 KW cardiant.

XX Homo sapiens.
 OS
 XX US2002169284-A1.
 PN
 XX 14-NOV-2002.
 PD

XX 16-OCT-2001; 2001US-0978697.
 XX
 XX 07-OCT-1998; 98WO-US21141.
 PR 20-NOV-1998; 98WO-US24855.
 PR 05-JAN-1999; 99WO-US00106.
 PR 08-MAR-1999; 99WO-US05028.
 PR 10-MAR-1999; 99WO-US05190.
 PR 14-MAY-1999; 99WO-US10733.
 PR 02-JUN-1999; 99WO-US12252.
 PR 30-NOV-1999; 99WO-US28313.
 PR 02-DEC-1999; 99WO-US28551.
 PR 02-DEC-1999; 99WO-US28565.
 PR 16-DEC-1999; 99WO-US30095.
 PR 30-DEC-1999; 99WO-US31243.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 10-MAR-2000; 2000WO-US06319.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 01-DEC-2000; 2000WO-US23678.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 22-MAR-2001; 2001WO-US09552.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 29-JUN-2001; 2001WO-US21066.
 PR 09-JUL-2001; 2001WO-US21735.
 PR 17-OCT-1997; 97US-062250B.
 PR 03-NOV-1997; 97US-064249F.
 PR 13-NOV-1997; 97US-065311B.
 PR 21-NOV-1997; 97US-066364F.
 PR 10-MAR-1998; 98US-077450D.
 PR 11-MAR-1998; 98US-077632P.
 PR 11-MAR-1998; 98US-077649F.
 PR 12-MAR-1998; 98US-077791B.
 PR 13-MAR-1998; 98US-078004P.
 PR 20-MAR-1998; 98US-078886F.
 PR 20-MAR-1998; 98US-078910F.
 PR 20-MAR-1998; 98US-078936P.
 PR 20-MAR-1998; 98US-078939F.
 PR 25-MAR-1998; 98US-079294F.
 PR 26-MAR-1998; 98US-079656P.
 PR 27-MAR-1998; 98US-079663P.
 PR 27-MAR-1998; 98US-079664P.
 PR 27-MAR-1998; 98US-079689P.
 PR 27-MAR-1998; 98US-079728P.
 PR 27-MAR-1998; 98US-079786F.
 PR 30-MAR-1998; 98US-079920P.
 PR 30-MAR-1998; 98US-079923P.
 PR 26-MAY-1981; 81US-0267213.
 PR 17-MAR-1998; 98US-00404220.
 PR 26-JUN-1998; 98US-0105413.
 PR 07-OCT-1998; 98US-0168978.
 PR 02-NOV-1998; 98US-0184216.
 PR 06-NOV-1998; 98US-0187358.
 PR 07-DEC-1998; 98US-0202054.
 PR 22-DEC-1998; 98US-0218517.
 PR 05-MAR-1999; 99US-0254465.

PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 29-JUN-2001; 2001WO-US21066.
 PR 09-JUL-2001; 2001WO-US21735.
 PR 17-OCT-1997; 97US-062250P.
 PR 03-NOV-1997; 97US-064249P.
 PR 13-NOV-1997; 97US-065311P.
 PR 21-NOV-1997; 97US-066364P.
 PR 10-MAR-1998; 98US-077450P.
 PR 11-MAR-1998; 98US-077632P.
 PR 11-MAR-1998; 98US-077641P.
 PR 12-MAR-1998; 98US-077791P.
 PR 13-MAR-1998; 98US-078004P.
 PR 20-MAR-1998; 98US-078886P.
 PR 20-MAR-1998; 98US-078910P.
 PR 20-MAR-1998; 98US-078936P.
 PR 20-MAR-1998; 98US-078939P.
 PR 25-MAR-1998; 98US-0792294P.
 PR 26-MAR-1998; 98US-079665P.
 PR 27-MAR-1998; 98US-079666P.
 PR 27-MAR-1998; 98US-079664P.
 PR 27-MAR-1998; 98US-079689P.
 PR 27-MAR-1998; 98US-079728P.
 PR 27-MAR-1998; 98US-079786P.
 PR 30-MAR-1998; 98US-079920P.
 PR 30-MAR-1998; 98US-079923P.
 PR 26-MAY-1981; 81US-0267213.
 PR 17-MAR-1998; 98US-0040220.
 PR 26-JUN-1998; 98US-0105413.
 PR 07-OCT-1998; 98US-0168978.
 PR 02-NOV-1998; 98US-0184216.
 PR 06-NOV-1998; 98US-0187368.
 PR 07-DEC-1998; 98US-0202054.
 PR 22-DEC-1998; 98US-0218517.
 PR 05-MAR-1999; 99US-0254465.
 PR 10-MAR-1999; 99US-0265686.
 PR 12-APR-1999; 99US-02844291.
 PR 14-MAY-1999; 99US-0311832.
 PR 14-MAY-1999; 99US-0380137.
 PR 25-AUG-1999; 99US-0380138.
 PR 25-AUG-1999; 99US-0380142.
 PR 08-NOV-2000; 2000US-0709238.
 PR 27-NOV-2000; 2000US-0723749.
 PR 20-DEC-2000; 2000US-0747259.
 PR 22-MAR-2001; 2001US-0816744.
 PR 22-MAR-2001; 2001US-0816920.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 01-JUN-2001; 2001US-0872035.
 PR 05-JUN-2001; 2001US-0874503.
 PR 14-JUN-2001; 2001US-0882536.
 PR 19-JUN-2001; 2001US-0886342.
 PR 30-JUL-2001; 2001US-0918585.
 XX
 PA (GETH) GENENTECH INC.
 XX

PI Ashkenazi A, Baker KP, Botstein D, Desnoyers L, Eaton D,
 PI Ferreira N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME,
 PI Goddard A, Godowski PJ, Grimaldi JC, Gurney AL, Hillan KJ,
 PI Kijavina J, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA,
 PI Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
 XX
 DR WPI: 2003-288163/28.
 DR N-PSDB; ABX92684.
 XX

PT Novel secreted and transmembrane polypeptides and polynucleotides
 PT encoding them useful for treating cancer, kidney diseases, bone,
 PT cartilage disorders and immune deficiencies
 XX
 XX Claim 12; Fig 215; 459pp; English.
 CC The present invention relates to the isolation of novel human PRO

CC polypeptides, and the polynucleotide sequences encoding them. The
 CC PRO polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides are useful for detecting other PRO polypeptides, for
 CC linking bioactive molecules to cells expressing PRO polypeptides,
 CC for modulating biological activities of cells expressing PRO
 CC polypeptides, and for identifying agonists or antagonists. The
 CC bioactive molecule may be a toxin, radiolabel or antibody, and causes
 CC apoptosis or death of the cell. The PRO polypeptides are useful for
 CC treating immune disorders, diabetes or hyper- or hypo-insulinaemia,
 CC cardiac insufficiency, nervous system disorders, kidney disorders,
 CC bone and cartilage disorders or arthritis, tumours, and wound healing.
 CC The polynucleotide sequences encoding PRO polypeptides are useful as
 CC hybridisation probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, in the preparation of PRO polypeptides, for
 CC generating transgenic animals or knockout animals, for the genetic
 CC analysis of individuals with genetic disorders, and in gene therapy.
 CC ABU61071-ABU61164 represent the human PRO polypeptides of the
 CC invention.
 CC Note: The sequence data for this patent was obtained in electronic
 CC format directly from the USPTO web site at
 CC seqdata.uspto.gov/psipdbidentry.html.
 CC
 CC Sequence 273 AA;
 SQ
 Query Match 100.0%; Score 1505; DB 24; Length 273;
 Best Local Similarity 100.0%; Pred. No. 5-5e-95;
 Matches 273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRSQEVLLMMLVLA VAGSTEHAYRGRVCAVRAHDPVSESFVQRYVYQPEPLTTCDDHR 60
 1 MRSQEVLLMMLVLA VAGSTEHAYRGRVCAVRAHDPVSESFVQRYVYQPEPLTTCDDHR 60
 Db 61 AGSTRRTTYRTPAYRRSPGLAARPRRYACCPGWRKRYSGLPAGCAATCCPPCRNGSSCVQP 120
 61 ACGSTRRTTYRTPAYRRSPGLAARPRRYACCPGWRKRYSGLPAGCAATCCPPCRNGSSCVQP 120
 Db 61 ACGSTRRTTYRTPAYRRSPGLAARPRRYACCPGWRKRYSGLPAGCAATCCPPCRNGSSCVQP 120
 121 GRCRCPAGWRGDTCCSDVDECSARRGGCPORCINTAGSYWCQCEWGHSLADGTLCPVKG 180
 121 GRCRCPAGWRGDTCCSDVDECSARRGGCPORCINTAGSYWCQCEWGHSLADGTLCPVKG 180
 Db 121 GRCRCPAGWRGDTCCSDVDECSARRGGCPORCINTAGSYWCQCEWGHSLADGTLCPVKG 180
 181 GPPRVA PNPVTGVDSAMKEEVORLQSRVLLBEKQLVLA PPHSLASQALHEHGLDPDPSGLL 240
 181 GPPRVA PNPVTGVDSAMKEEVORLQSRVLLBEKQLVLA PPHSLASQALHEHGLDPDPSGLL 240
 Db 181 GPPRVA PNPVTGVDSAMKEEVORLQSRVLLBEKQLVLA PPHSLASQALHEHGLDPDPSGLL 240
 241 VHSFOQLGRIDSLSEQISFLEBQLSSCSCKKDS 273
 241 VHSFOQLGRIDSLSEQISFLEBQLSSCSCKKDS 273
 QY
 Db
 RESULT 14
 AAY41771
 ID AAY41771 standard; Protein; 273 AA.
 AC AAY41771;
 XX
 DT 07-DEC-1999 (first entry)
 XX
 DE Human PRO1449 protein sequence.
 XX
 KW Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;
 KW probe; blood coagulation disorder; cancer; cellular adhesion disorder;
 KW secreted protein; transmembrane protein.
 XX
 OS Homo sapiens.
 XX
 PN WO9946281-A2.
 XX
 PD 16-SEP-1999.
 XX
 PF 08-MAR-1999; 99WO-US05028.
 XX
 PR 10-MAR-1998; 98US-0077450.
 XX
 PR 11-MAR-1998; 98US-0077632.

PR 11-MAR-1998; 98US-0077641.
 PR 11-MAR-1998; 98US-0077649.
 PR 12-MAR-1998; 98US-0077791.
 PR 13-MAR-1998; 98US-0078004.
 PR 17-MAR-1998; 98US-0040220.
 PR 20-MAR-1998; 98US-0078886.
 PR 20-MAR-1998; 98US-0078910.
 PR 20-MAR-1998; 98US-0078936.
 PR 25-MAR-1998; 98US-0078939.
 PR 26-MAR-1998; 98US-0079294.
 PR 27-MAR-1998; 98US-0079663.
 PR 27-MAR-1998; 98US-0079664.
 PR 27-MAR-1998; 98US-0079689.
 PR 27-MAR-1998; 98US-0079728.
 PR 27-MAR-1998; 98US-0079786.
 PR 30-MAR-1998; 98US-0079920.
 PR 30-MAR-1998; 98US-0079923.
 PR 31-MAR-1998; 98US-0080105.
 PR 31-MAR-1998; 98US-0080107.
 PR 31-MAR-1998; 98US-0080165.
 PR 31-MAR-1998; 98US-0080194.
 PR 01-APR-1998; 98US-0080327.
 PR 01-APR-1998; 98US-0080328.
 PR 01-APR-1998; 98US-0080333.
 PR 01-APR-1998; 98US-0080334.
 PR 08-APR-1998; 98US-0081049.
 PR 08-APR-1998; 98US-0081070.
 PR 08-APR-1998; 98US-0081071.
 PR 09-APR-1998; 98US-0081195.
 PR 09-APR-1998; 98US-0081203.
 PR 09-APR-1998; 98US-0081229.
 PR 15-APR-1998; 98US-0081817.
 PR 15-APR-1998; 98US-0081838.
 PR 15-APR-1998; 98US-0081952.
 PR 15-APR-1998; 98US-0081955.
 PR 21-APR-1998; 98US-0082568.
 PR 21-APR-1998; 98US-0082569.
 PR 22-APR-1998; 98US-0082700.
 PR 22-APR-1998; 98US-0082704.
 PR 22-APR-1998; 98US-0082804.
 PR 23-APR-1998; 98US-0082767.
 PR 23-APR-1998; 98US-0082796.
 PR 27-APR-1998; 98US-0083336.
 PR 28-APR-1998; 98US-0083332.
 PR 29-APR-1998; 98US-0083392.
 PR 29-APR-1998; 98US-0083495.
 PR 29-APR-1998; 98US-0083496.
 PR 29-APR-1998; 98US-0083499.
 PR 29-APR-1998; 98US-0083500.
 PR 29-APR-1998; 98US-0083545.
 PR 29-APR-1998; 98US-0083545.
 PR 29-APR-1998; 98US-0083554.
 PR 29-APR-1998; 98US-0083558.
 PR 30-APR-1998; 98US-0083559.
 PR 05-MAY-1998; 98US-0083742.
 PR 06-MAY-1998; 98US-0084366.
 PR 06-MAY-1998; 98US-0084414.
 PR 06-MAY-1998; 98US-0084441.
 PR 07-MAY-1998; 98US-0084598.
 PR 07-MAY-1998; 98US-0084600.
 PR 07-MAY-1998; 98US-0084627.
 PR 07-MAY-1998; 98US-0084637.
 PR 07-MAY-1998; 98US-0084639.
 PR 07-MAY-1998; 98US-0084640.
 PR 07-MAY-1998; 98US-0084643.
 PR 13-MAY-1998; 98US-0085323.
 PR 13-MAY-1998; 98US-0085338.
 PR 13-MAY-1998; 98US-0085339.
 PR 15-MAY-1998; 98US-0085573.
 PR 15-MAY-1998; 98US-0085579.
 PR 15-MAY-1998; 98US-0085580.
 PR 15-MAY-1998; 98US-0085582.
 PR 15-MAY-1998; 98US-0085689.

PR 15-MAY-1998; 98US-0085697.
 PR 15-MAY-1998; 98US-0085700.
 PR 15-MAY-1998; 98US-0085704.
 PR 18-MAY-1998; 98US-0086023.
 PR 22-MAY-1998; 98US-0086392.
 PR 22-MAY-1998; 98US-0086414.
 PR 22-MAY-1998; 98US-0086430.
 PR 22-MAY-1998; 98US-0086430.
 PR 28-MAY-1998; 98US-0086486.
 PR 28-MAY-1998; 98US-0087098.
 PR 28-MAY-1998; 98US-0087106.
 PR 28-MAY-1998; 98US-0087208.
 PR 30-JUL-1998; 98US-0094651.
 PR 11-SEP-1998; 98US-0100038.
 PA (GENH) GENENTECH INC.
 XX Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
 XX WPI, 1999-551358/46.
 DR N-PSDB; AAZ34313.
 XX
 PT New secreted and transmembrane polypeptides and their polynucleotides,
 FT useful for treating blood coagulation disorders, cancers and cellular
 PT adhesion disorders
 XX
 XX
 PS Claim 12; Fig 217; 530pp; English.
 CC The present invention describes secreted and transmembrane polypeptides
 CC and their polynucleotides. The nucleotide sequences are useful as
 CC sources of probes, primers, for chromosome mapping, and for generation
 CC of antisense sequences. They can also be used to create transgenic
 CC animals. The proteins can be used to treat a variety of diseases and
 CC disorders, depending on their function. Diseases that may be treated
 CC include blood coagulation disorders, cancers and cellular adhesion
 CC disorders. They may also be used to raise antibodies. AAZ33891 to
 CC AAZ34338, and AA41685 to AA41774 represent polynucleotide and
 CC polypeptide sequence given in the exemplification of the present
 CC invention.
 XX
 XX Sequence 273 AA;
 SO
 Query Match 99.9%; Score 1504; DB 20; Length 273;
 Best Local Similarity 99.6%; Pred. No. 6.4e-95;
 Matches 272; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 OY 1 MRGQEVLLMVLVAVGTEHAYRPGRRVCAVAHADDVSESVQRYVQPELTTCDGHR 60
 1 MRGQEVLLMVLVAVGTEHAYRPGRRVCAVAHADDVSESVQRYVQPELTTCDGHR 60
 Db 1 MRGQEVLLMVLVAVGTEHAYRPGRRVCAVAHADDVSESVQRYVQPELTTCDGHR 60
 OY 61 ACSYRRTYRTPAVRSGGLAPRPRVYACCPGKRTSGLPACGAAITQPPCRNGSCVOP 120
 61 ACSYRRTYRTPAVRSGGLAPRPRVYACCPGKRTSGLPACGAAITQPPCRNGSCVOP 120
 Db 61 ACSYRRTYRTPAVRSGGLAPRPRVYACCPGKRTSGLPACGAAITQPPCRNGSCVOP 120
 OY 121 GRCCPAGMRGDTQSDVDDECSARSGCPCORCINTAGSYWCCWEGHSLADGTLVCPKG 180
 121 GRCCPAGMRGDTQSDVDDECSARSGCPCORCINTAGSYWCCWEGHSLADGTLVCPKG 180
 Db 121 GRCCPAGMRGDTQSDVDDECSARSGCPCORCINTAGSYWCCWEGHSLADGTLVCPKG 180
 OY 181 GPPRVANPPTGVDSAMKEEVQRLQSRVLDLEKQLVLAHLSIASQALBHGJLPPDPSLL 240
 181 GPPRVANPPTGVDSAMKEEVQRLQSRVLDLEKQLVLAHLSIASQALBHGJLPPDPSLL 240
 Db 181 GPPRVANPPTGVDSAMKEEVQRLQSRVLDLEKQLVLAHLSIASQALBHGJLPPDPSLL 240
 OY 241 VHSFOQLGRIDSLSBOISFLEBOLGSCCKKDS 273
 241 VHSFOQLGRIDSLSBOISFLEBOLGSCCKKDS 273
 Db 241 VHSFOQLGRIDSLSBOISFLEBOLGSCCKKDS 273
 RESULT 15
 AA08381
 ID AA08381 standard; Protein: 273 AA.
 XX AA08381;
 AC AA08381;
 AC AA08381;
 XX 26-APR-1999 (first entry)
 DT

XX DE Human neuro-growth factor-like protein Zneul.
 XX KW Zneul-1; neuro-growth factor-like protein; human; breast cancer;
 KW glioblastoma; pituitary adenoma; Alzheimer's disease; therapy;
 KM nerve regeneration; haematopoiesis; fertility; contraception;
 KM antibody.
 XX OS Homo sapiens.
 XX FH Key Location/Qualifiers
 FH Peptide 1..19
 FT /note= "putative signal peptide"
 FT Protein 20..273
 FT /note= "mature protein"
 FT Domain 20..104
 FT /note= "hydrophilic domain (HSM1), homologous to
 FT an HSMHC3W5A domain "
 FT Domain 105..135
 FT /note= "epidermal growth factor-like domain 1"
 FT Domain 135..177
 FT /note= "epidermal growth factor-like domain 2"
 FT Domain 178..273
 FT /note= "domain HSM2 homologous to an HSMHC3W5A
 FT domain"
 XX PN W09857983-A2.
 XX PD 23-DEC-1998.
 XX PR 18-JUN-1998; 98WO-US12763.
 XX PR 18-JUN-1997; 97US-0878322.
 XX PR 18-JUN-1997; 97US-0050143.
 XX PA (ZYMO) ZYMOGENETICS INC.
 XX PI Blumberg H, Jelinek LJ, Lehner JM, Sheppard PO;
 XX PI Whitmore TE;
 XX DR MPI; 1999-095324/08.
 XX DR N-PSDB; AAV84341.
 XX PS Claim 6; Page 47-48; 70pp; English.
 CC This polypeptide comprises human Zneul, a new neuro-growth factor-
 CC like protein. Its amino acid sequence was deduced from the
 CC nucleotide sequence (see AAV84341) of a cDNA clone isolated from a
 CC brain cDNA library. Zneul's closest human homologue is HSMHC3W5A,
 CC a gene in the HLA class III region, which is contained in a cosmid
 CC which contains Notch 4. Zneul is also homologous to Notch 4 in its
 CC EGF-like domains and may be involved in EGF receptor pathways.
 CC Zneul is widely expressed in adult tissues, with high expression in
 CC heart, placenta, spleen, testis, thyroid, spinal cord and lymph
 CC node. Zneul polypeptide can be used as a growth, maintenance, or
 CC differentiation factor in the spinal cord, heart, spleen, testis,
 CC thyroid and lymph nodes. It may also play a role in breast cancer,
 CC glioblastomas, and pituitary adenomas. Zneul may be used to treat
 CC Alzheimer's disease, cancer, to repopulate blood cells after
 CC chemotherapy, to stimulate myofibroblast proliferation, stimulate
 CC or inhibit growth factors made in the placenta, in fertility and
 CC contraction, or to regenerate nerves. Claimed Zneul
 CC polypeptides (see also AAV88382-97), including specific domains of
 CC Zneul and epitope-bearing portions of Zneul, can be used to raise
 CC specific antibodies for use e.g. in diagnostic assays.
 XX SQ Sequence 273 AA;

Query Match 99.9%; Score 1504; DB 20; Length 273;
 Best Local Similarity 99.6%; Pred. No. 6.4e-95;

Matches	Conservative	1;	Mismatches	0;	Indels	0;	Gaps	0;																	
QY	1	MRGSEVLLMLLVLA	VGTEHAYR	QVRAHGD	PVSESFVQRY	YQPF	LTTC	DGHR 60																	
Db	1	MRGSEVLLMLLVLA	VGTEHAYR	QVRAHGD	PVSESFVQRY	YQPF	LTTC	DGHR 60																	
QY	61	ACSTYRTTYRTA	YRRSPGLA	PARPRY	ACCPG	WKR	TSSG	IPGACGAAICQPPCRANGSSCVQ 120																	
Db	61	ACSTYRTTYRTA	YRRSPGLA	PARPRY	ACCPG	WKR	TSSG	IPGACGAAICQPPCRANGSSCVQ 120																	
QY	121	GRCP	PAGWRG	BDT	CS	DVDE	CS	ARRG	GPCRCINT	PAGSYWCQ	MEGHSLS	ADGT	CV	PKG 180											
Db	121	GRCP	PAGWRG	BDT	CS	DVDE	CS	ARRG	GPCRCINT	PAGSYWCQ	MEGHSLS	ADGT	CV	PKG 180											
QY	181	GPPRVA	PMP	PTG	VDS	AMKEE	VOR	LQ	SR	VD	L	BE	KLQ	LV	LA	PL	HS	LA	SQ	AL	EH	GL	PD	PS	LL 240
Db	181	GPPRVA	PMP	PTG	VDS	AMKEE	VOR	LQ	SR	VD	L	BE	KLQ	LV	LA	PL	HS	LA	SQ	AL	EH	GL	PD	PS	LL 240
QY	241	VHS	FQ	DL	GR	IDS	LS	EQ	IS	FL	EB	QL	SS	CS	CK	DS 273									
Db	241	VHS	FQ	DL	GR	IDS	LS	EQ	IS	FL	EB	QL	SS	CS	CK	DS 273									

Search completed: September 10, 2003, 17:13:01
 Job time : 87 secs